

<210> 329
 <211> 585
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 331..432

<221> sig_peptide
 <222> 331..387
 <223> Von Heijne matrix
 score 7
 seq AGLSSCLLPLCWL/ER

<221> polyA_signal
 <222> 548..553

<221> polyA_site
 <222> 573..585

<400> 329
 aagcctaggt gtggcgcccc gaccggactt tcacttctgg ccagcccttt cccacactgg 60
 gcgcgggass ggtgccagtc tttaacaac ctctcgatgg gtcccacgaa gatgtttcca 120
 gacccttgga atgccaagtt caagttagc tatgtctcgc ggagaggccg gtggaagaag 180
 caacgagaat gaagcaccac agttctctgc tgagcacatg ggcactctgca ataaagattt 240
 aatttcccag cttctcctga agtcgggtat ggccacaaca cttaaattctg cccgaggaga 300
 ttgagcaaaa tagtatggga cttccaagaa atg ttt tta aag tca ggg gca ggc 354
 Met Phe Leu Lys Ser Gly Ala Gly
 -15
 ctt tct tca tgc ctt ctt cct ctt tgc tgg ctg gaa cgc aaa gac cat 402
 Leu Ser Ser Cys Leu Leu Pro Leu Cys Trp Leu Glu Arg Lys Asp His
 -10 -5 1 5
 ggc agg agg cca agc asc cat cct gga agg tgaaagcctc atactaagga 452
 Gly Arg Arg Pro Ser Xaa His Pro Gly Arg
 10 15
 cgtcaracag cgaaataara rcctgggtcc ttgaccctgt aaasatctcc ctccccatcc 512
 tggctctgtc gccttgactc ctttcatatg aaaaaaataa acttttaact tgcgtwaacc 572
 aaaaaaaaaa aaa 585

<210> 330
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 <212> DNA
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<220>
 <221> CDS
 <222> 59..703

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 <222> 59..220
 <223> Von Heijne matrix
 score 5.099999990463257
 seq FLLSQMSQHQA/VQ

<221> polyA_signal
 <222> 886..891

<221> polyA_site

<222> 903..914

<400> 330

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acaaatatca atgatgttta tgaatctagt gtgaaagtkt taatcacatc acaaggct      58
atg aac rra tat gca agt cca ttc aac tgw caa ttg ard tat ttg gak      106
Met Asn Xaa Tyr Ala Ser Pro Phe Asn Xaa Gln Leu Xaa Tyr Leu Xaa
      -50      -45      -40
ttg agc agr ttc gag tgt gtr cat aga gat gga aga gta att aca ctg      154
Leu Ser Arg Phe Glu Cys Val His Arg Asp Gly Arg Val Ile Thr Leu
      -35      -30      -25
tct tat cag gag cag gag cta cag gat ttt ctt ctg tct cag atg tca      202
Ser Tyr Gln Glu Gln Glu Leu Gln Asp Phe Leu Leu Ser Gln Met Ser
      -20      -15      -10
cag cac cag gta cat gca gtt cag caa ctc gcc aag gtt atg ggc tgg      250
Gln His Gln Val His Ala Val Gln Gln Leu Ala Lys Val Met Gly Trp
      -5      1      5      10
caa gta ctg agc ttc agt aat cat gtg gga ctt gga cct ata gag agc      298
Gln Val Leu Ser Phe Ser Asn His Val Gly Leu Gly Pro Ile Glu Ser
      15      20      25
abt ggt aat gca tct gcc atc acg gtg gcc ccc caa gtg gtg act atg      346
Xaa Gly Asn Ala Ser Ala Ile Thr Val Ala Pro Gln Val Val Thr Met
      30      35      40
cta ttt cag ttc gta atg gac ctg aaa gtg gca gca aga tta tgg ttc      394
Leu Phe Gln Phe Val Met Asp Leu Lys Val Ala Ala Arg Leu Trp Phe
      45      50      55
agt ttc ctc gta acc aat gta aar acc ttc caa aaa gtg atg ttt tac      442
Ser Phe Leu Val Thr Asn Val Lys Thr Phe Gln Lys Val Met Phe Tyr
      60      65      70
aar ata aca aat gga gtc atc ttc gtg gcc cat tca aar aag ttc agt      490
Lys Ile Thr Asn Gly Val Ile Phe Val Gly His Ser Lys Lys Phe Ser
      75      80      85      90
gga ata aaa tgg aag gtc kaa att ttg ttt ata aaa tgg arm tgc tta      538
Gly Ile Lys Trp Lys Val Xaa Ile Leu Phe Ile Lys Trp Xaa Cys Leu
      95      100      105
tgt ctg cac tta gcc ctt gtc tac tat gat ttt ttc car atg ttt cct      586
Cys Leu His Leu Ala Leu Val Tyr Tyr Asp Phe Phe Gln Met Phe Pro
      110      115      120
aaa raa gtt tcc ara aac ttt gac ttg aaa tgt ttg car atc aac tat      634
Lys Xaa Val Ser Xaa Asn Phe Asp Leu Lys Cys Leu Gln Ile Asn Tyr
      125      130      135
aag cac aaa gaa gar ata act tcc aaa aga gtg ctg ttt tta aaa ata      682
Lys His Lys Glu Glu Ile Thr Ser Lys Arg Val Leu Phe Leu Lys Ile
      140      145      150
ata att agg aaa tgt ttt att tagcactttc aaacttttca ctttataaat      733
Ile Ile Arg Lys Cys Phe Ile
155      160
gacaagtgtt ttgaaatgca gaagtttatg tacagttgta tatacagtat gacaagatgt      793
aaaataatat gtttttcatg cagtttaaaa tattactaac ttaagggttt ctatgtgctt      853
tttaaaatat tccttctttg atgttgacat caaataaagt atgtgggttta aaaaaaaaaa      913
a                                                                 914

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<210> 331

<211> 1161

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<213> Homo sapiens

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<221> CDS

<222> 672..752

<221> sig_peptide
 <222> 672..722
 <223> Von Heijne matrix
 score 4.30000019073486
 seq LLYAHLSTSKRA/VV

<221> polyA_site
 <222> 1150..1161

<400> 331
 aagatatcac tgtcttgttt tcacttagat cctacttaca aagtgagggt tattaacaga 60
 ataaagcctt cctttaagc tttataataa tcatatttat taataatgct gttgtgcata 120
 cttatagtat gcatatatc agcatatggt gcatgtsttc agaattacat aagatgaaat 180
 ccctttcatt gcaacttgca agtgagaaaa gatccttagt ggctctggtg gaagaaatag 240
 tatttcttct tctcagggtg tctccctgcc ttggccctc ccagaagccc cggctttaaa 300
 agtgaaaatg tttgaaacat gaaacatgtc tgtaggaagc atcagcatgg ccataagtg 360
 artgattttc atatatgcct ctgcccattt caaatatatt tttgacatga ataaatctaa 420
 cagtatacar aataattcat gtaaraccct aacgtgtaca tgtgaaaaag catttctata 480
 taatgtgagg agcactggcc atcaattagg gaaataaagg tcatgtaata ttgcaaattt 540
 tcaaaataga gcsstgcaag ataaactgca tcataccaaa aactatttga gtaaatggat 600
 ttttaaagta atttttgttt aaaaaaattt atatttcaga agsagaaaaat gtcaaatgat 660
 agtctttgta a atg gtg gtg cac ctt ctc tat gca cat ctg tct ttt aca 710
 Met Val Val His Leu Leu Tyr Ala His Leu Ser Phe Thr
 -15 -10 -5
 tca aaa aga gct gtg gtc atg cta aaa tta gag ata act ttt 752
 Ser Lys Arg Ala Val Val Met Leu Lys Leu Glu Ile Thr Phe
 1 5 10
 tgaatgactt ggtcaagctg tgtgtaaaat atttaaccat aagtcaagta cagtgtacta 812
 tgtttaataa agttacattt aatgcattta ttgcatatat gaatatatac atgaagaggc 872
 tttatgtctt ctgggtatttg attttgaatg ttttttaagt cagtgggtgcc tttaggcaag 932
 aactttcgaa attaatcatt ctttgtgttt tctgattttt caggtaacat gtacactatt 992
 tagaaacat catagtttat tcaccttaaa aaattgattg tattatttaa atatatcact 1052
 tagatgggca tttcctataa ttaggatatt ccaaatagtt gctgaaatca attgtgccat 1112
 tgaccaatgg atgcacttgg ttagccttaa ttttttyaaa aaaaaaaaaa 1161

<210> 332
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 <212> DNA
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<220>
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 <222> 57..311

<221> sig_peptide
 <222> 57..128
 <223> Von Heijne matrix
 score 5.30000019073486
 seq LFHLLFLPHYIET/FK

<221> polyA_signal
 <222> 332..337

<221> polyA_site
 <222> 351..363

<400> 332
 acatttctta ctgccttacg ctcacctga ggtccacett ggtctctaaa aacacc atg 59
 Met

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tgt tct cat gcc tcc atg tct ttt cac aca ctg ttc cat ttg ctc ttc      107
Cys Ser His Ala Ser Met Ser Phe His Thr Leu Phe His Leu Leu Phe
      -20                      -15                      -10
ctc cca cat tac att gaa act ttc aag cct cag tcg aaa cat tgc ttc      155
Leu Pro His Tyr Ile Glu Thr Phe Lys Pro Gln Ser Lys His Cys Phe
      -5                      1                      5
ttc tgg ata gca gcc ttc ttg aca tcc ctc ctc act ccc cag tcc cta      203
Phe Trp Ile Ala Ala Phe Leu Thr Ser Leu Leu Thr Pro Gln Ser Leu
10                      15                      20                      25
cag ggc ttc cat agc tct tta tgt gca ctt cga tcc cag cat ttt cca      251
Gln Gly Phe His Ser Ser Leu Cys Ala Leu Arg Ser Gln His Phe Pro
      30                      35                      40
tcg act tgt aat tgt ttc tgc tac ctg aca atc atc gcc ttg drd tac      299
Ser Thr Cys Asn Cys Phe Cys Tyr Leu Thr Ile Ile Ala Leu Xaa Tyr
      45                      50                      55
tgg gac aac ctt tgattactca ttatatcctc aataaatatt tgttgaacca      351
Trp Asp Asn Leu
60
aaaaaaaaaa aa      363

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<210> 333
 <211> 645
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..232

<221> sig_peptide
 <222> 80..127
 <223> Von Heijne matrix
 score 3.70000004768372
 seq IALTLIPMSLSRA/AG

<221> polyA_signal
 <222> 617..622

<221> polyA_site
 <222> 634..645

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<400> 333
accttcttgt tatatatget attctctttg tggtccatt cttctttcaa tcttctcagc      60
ttataaccgt ctttccctt atg cta agg ata gcc ctt aca ctc atc cca tct      112
                      Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser
                      -15                      -10
atg ctg tca agg gct gct ggt tgg tgc tgg tac aag gag ccc act cag      160
Met Leu Ser Arg Ala Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln
-5                      1                      5                      10
cag ttt tct tac ctt tgc ctg ccc tgc ctt tca tgg aat aar aaa ggc      208
Gln Phe Ser Tyr Leu Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly
      15                      20                      25
aac gtt ttg cag ctt cca aat ttc tgaaraaact aatctcarat tggcagttaa      262
Asn Val Leu Gln Leu Pro Asn Phe
      30                      35
agtcaaaatg ttgccaaata tttattcctt ttgcctaakt ttggctaccc ggttcaattg      322
ctttttatatt ttaatgtctt gactcttcar agttcgtacc tcaaaaraac aatgaraaca      382
tttgctttgc tttctgctga atccctaata tcaacaatct atacctggac tgtccagttc      442
tcctcctgtg ctatcttctc ttctatccaa gtaraatgta ygccaggarc tccttccctc      502
tarcaatttc tactaaaatg tccaagtara atgtttcctt ttacaatcaa attactgtat      562

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ttattaattt gctaraatcc aktaaactcat tttggtagct ctggctgtgc tatcaataaa 622
aagatgaaag caaaaaaaaaaaa aaa 645

<210> 334
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<212> DNA
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<221> CDS
<222> 91..291

<221> sig_peptide
<222> 91..219
<223> Von Heijne matrix
score 3.79999995231628
seq LISVLYLIPKTLT/TN

<221> polyA_signal
<222> 367..372

<221> polyA_site
<222> 389..400

<400> 334
aacaaaagga gagttttata attcacttta aaaggagatt tgatggtaaa gtttaaagat 60
taaaatattt tgttcttcaa ttacagagcg atg acc cca cag tat ctg cct cac 114
Met Thr Pro Gln Tyr Leu Pro His
-40
ggt gga aaa tac caa gtt ctt gga gat tac tct ttg gca gtg gtc ttc 162
Gly Gly Lys Tyr Gln Val Leu Gly Asp Tyr Ser Leu Ala Val Val Phe
-35 -30 -25 -20
ccc ctg cac ttt tct gat cta att tct gtt tta tac ctt ata ccc aaa 210
Pro Leu His Phe Ser Asp Leu Ile Ser Val Leu Tyr Leu Ile Pro Lys
-15 -10 -5
aca ctt act acc aac aca gct gtt aaa cat tct ata caa aaa aat tgt 258
Thr Leu Thr Thr Asn Thr Ala Val Lys His Ser Ile Gln Lys Asn Cys
1 5 10
atg mat ctg gta tta gga aaa tta ctt tca cag taaatatcaa agaaaaaaga 311
Met Xaa Leu Val Leu Gly Lys Leu Leu Ser Gln
15 20
ttaagggtct ctttgccatg cttttcatca tatgcaccaa atgtaaattt tgtacaataa 371
aattttattt cctaagyaaa aaaaaaaaaa 400

<210> 335
<211> 496
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 196..384

<221> sig_peptide
<222> 196..240
<223> Von Heijne matrix
score 6.69999980926514
seq ILSTVTALTFARA/LD

<221> polyA_signal

<222> 461..466

<221> polyA_site

<222> 485..496

<400> 335

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aaaaaattgg tcccagtttt caccctgccg cagggctggc tggggagggc agcgggttag      60
attagccgtg gcttaggccg ttttaacgggg tgacacgagc htgcagggcc gagtccaagg      120
cccggagata ggaccaaccg tcaggaatgc gaggaatggt tttcttcgga ctctatcgag      180
gcacacagac agacc atg ggg att ctg tct aca gtg aca gcc tta aca ttt      231
                Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
                -15                -10                -5
gcc aga gcc ctg gac ggc tgc aga aat ggc att gcc cac cct gca agt      279
Ala Arg Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
                1                5                10
gag aag cac aga ctc gag aaa tgt agg gaa ctc gag agc agc cac tcg      327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser
                15                20                25
gcc cca gga tca acc cag cac cga aga aaa aca acc aga aga aat tat      375
Ala Pro Gly Ser Thr Gln His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
                30                35                40                45
tct tca gcc tgaaatgaak ccgggatcaa atggttgctg atcaragccc      424
Ser Ser Ala
atattttaat tgaaaaagtc aaattgasca ttattaaata aagcttggtt aatatgtctc      484
aaacaaaaaa aa      496

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<210> 336

<211> 968

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 54..590

<221> sig_peptide

<222> 54..227

<223> Von Heijne matrix

score 3.5

seq GGILMGSFQGTIA/GQ

<221> polyA_site

<222> 955..965

<400> 336

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atatttgccc cttactttat cttgtgcctt gagaaattgc tggggagaga ggt atg      56
                Met
tcc act ggg cag ctg tac agg atg gag gat ata ggg cgt ttc cac tcc      104
Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His Ser
                -55                -50                -45
cag cag cca ggt tcc ctc acc cca agc tca ccc act gtt ggg gag att      152
Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu Ile
                -40                -35                -30
atc tac aat aac acc aga aac aca ttg ggg tgg att ggg ggt atc ctt      200
Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile Leu
                -25                -20                -15                -10
atg ggt tct ttt cag gga acc att gct gga caa ggc aca gga gcc acc      248
Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala Thr

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      -5              1              5
tcc att tct gag ctc tgc aag gga caa gaa cta gag cca tca ggg gct      296
Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly Ala
      10              15              20
ggg ctc act gtg gcc cca ccc caa gcc gtc agc ctc cag ggw atc tac      344
Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ile Tyr
      25              30              35
acc ctg cct tgg ctg cta cag ctt ttt cac tcc act gcc cta rgg gna      392
Thr Leu Pro Trp Leu Leu Gln Leu Phe His Ser Thr Ala Leu Xaa Xaa
      40              45              50              55
dtt cag caa cct aat gga tct cta tct ctg aac atc tct tca tcc cat      440
Xaa Gln Gln Pro Asn Gly Ser Leu Ser Leu Asn Ile Ser Ser Ser His
      60              65              70
gct ccr rgt cca rca acc tgc acc ctg gaa cca gga gtg gac cct acc      488
Ala Pro Xaa Pro Xaa Thr Cys Thr Leu Glu Pro Gly Val Asp Pro Thr
      75              80              85
cga sct gtc tgt att aat ccc cat ccc cca cca cca atc tta aaa abc      536
Arg Xaa Val Cys Ile Asn Pro His Pro Pro Pro Pro Ile Leu Lys Xaa
      90              95              100
cct ctg tcc ccc tac cct aaa ccc cag tta ggt acc cat gct ggg caa      584
Pro Leu Ser Pro Tyr Pro Lys Pro Gln Leu Gly Thr His Ala Gly Gln
      105              110              115
gtc aat taacaattta tgcacaggta ctagtatttat tgtattaccg ttccagggtgta      640
Val Asn
120
gctttgaaaa aagtatctca aaaaggcaac atgggcccag cgcagtggct cacgcctgta      700
atcccagcac tttgggaggc caaggtgggc agatcgctg aggtctggag ttcaagacca      760
gcctggccaa caggggtgaaa ccccgctctet acaaaaatar gaaaatttrgc caggtgtggt      820
ggcagacgtc tgtrgtccca gctattcagg agactgaggc acgagaattc catgaaccca      880
ggatgcggag gttgcagtga gccgagattg tgccactgcg ctccagcctg ggcgacagag      940
tggtattctg tttcaaaaaa aaaaamcm      968

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<210> 337
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 133..846

<221> sig_peptide
 <222> 133..345
 <223> Von Heijne matrix
 score 9.39999961853027
 seq VVSFLLLLAGLIA/TY

<221> polyA_site
 <222> 890..901

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<400> 337
aagcagcttc caggatcctg agatccggag cagccgggggt cggagcggct cctcaagagt      60
tactgatcta tnnatggcag agaaaaaaaa attgtgacca gagacgtgta gcaatgaaca      120
aggaacrta ta atg rwm nnk ttc aca gac ccc tct tca gtg aat gaa aag      171
      Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys
      -70              -65              -60
aag agg agg gag cgg gaa gaa agg cag aat att gtc ctg tgg aga cag      219
Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln
      -55              -50              -45
ccg ctc att acc ttg cag tat ttt tct ctg gaa atc ctt gta atc ttg      267

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Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu
-40 -35 -30
aag gaa tgg acc tca aaa tta tgg cat cgt caa agc att gtg gtg tct 315
Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser
-25 -20 -15
ttt tta ctg ctg ctt gct ggg ctt ata gct acg tat tat gtt gaa gga 363
Phe Leu Leu Leu Leu Ala Gly Leu Ile Ala Thr Tyr Tyr Val Glu Gly
-10 -5 1 5
gtg cat caa cag tat gtg caa cgt ata gag aaa cag ttt ctt ttg tat 411
Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr
10 15 20
gcc tac tgg ata ggc tta gga att ttg tct tct gtt ggg ctt gga aca 459
Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr
25 30 35
ggg ctg cac acc ttt ctg ctt tat ctg ggt cca cat ata gcc tca gtt 507
Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val
40 45 50
aca tta gct gct tat gaa tgc aat tca gtt aat ttt ccc gaa cca ccc 555
Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro
55 60 65 70
tat cct gat cag att att tgt cca gat gaa gag ggc act gaa gga acc 603
Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr
75 80 85
att tct ttg tgg agt atc atc tca aaa gtt agg att gaa gcc tgc atg 651
Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met
90 95 100
tgg ggt atc ggt aca gca atc gga gag ctg cct cca tat ttc atg gcc 699
Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala
105 110 115
aga gca gct cgc ctc tca ggt gct gaa cca gat gat gaa gag tat cag 747
Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln
120 125 130
gaa ttt gaa gag atg ctg gaa cat gca gag tct gca caa gta aga aca 795
Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Val Arg Thr
135 140 145 150
gtg ggg ata gaa aat aga aca ctt tac ttc ttc cta aag agg cta tta 843
Val Gly Ile Glu Asn Arg Thr Leu Tyr Phe Phe Leu Lys Arg Leu Leu
155 160 165
agg taaaattggt agtagttact ctgaagaaga aaactgctaa agtaaaaaaa aaaaa 901
Arg

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<210> 338

<211> 1347

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 138..671

<221> sig_peptide

<222> 138..248

<223> Von Heijne matrix

score 3.5

seq LVFNFLILITILT/IW

<221> polyA_signal

<222> 1319..1324

<221> polyA_site

<222> 1338..1347

<400> 338

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aagaatgctt gtgaagtagc aactaaagtg gcagtgtttc ttctgaaatt ctcaggcagt      60
cagactgtct taggcaaate ttgataaaat agcccttatac cagggttttta tctaaggaat    120
cccaagaaga ctggggga atg gag aga cag tca agg gtt atg tca gaa aag        170
                Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys
                -35                                -30
gat gag tat cag ttt caa cat cag gga gcg gtg gag ctg ctt gtc ttc      218
Asp Glu Tyr Gln Phe Gln His Gln Gly Ala Val Glu Leu Leu Val Phe
-25                                -20                                -15
aat ttt ttg ctc atc ctt acc att ttg aca atc tgg tta ttt aaa aat      266
Asn Phe Leu Leu Ile Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn
-10                                -5                                1                                5
cat cga ttc cgc ttc ttg cat gaa act gga gga gca atg gtg tat ggc      314
His Arg Phe Arg Phe Leu His Glu Thr Gly Gly Ala Met Val Tyr Gly
10                                15                                20
ctt aya atg gga cta att tta csa tat gct aca gca cca act gat att      362
Leu Xaa Met Gly Leu Ile Leu Xaa Tyr Ala Thr Ala Pro Thr Asp Ile
25                                30                                35
gaa agt ggr rct gtc tat gac tgt gta aaa cta act ttc agt cca tca      410
Glu Ser Gly Xaa Val Tyr Asp Cys Val Lys Leu Thr Phe Ser Pro Ser
40                                45                                50
act ctg ctg gtt aat atc act gac caa gtt tat gar tat aaa tac aar      458
Thr Leu Leu Val Asn Ile Thr Asp Gln Val Tyr Glu Tyr Lys Tyr Lys
55                                60                                65                                70
aga gaa ata agt cag cac amc atc aat cct cat cam gga aat gct ata      506
Arg Glu Ile Ser Gln His Xaa Ile Asn Pro His Xaa Gly Asn Ala Ile
75                                80                                85
ctt gaa aag atg aca ttt gat cca raa atc ttc ttc aat gtt tta ctg      554
Leu Glu Lys Met Thr Phe Asp Pro Xaa Ile Phe Phe Asn Val Leu Leu
90                                95                                100
cca cca att ata ttt cat gca gga tat agt cta aag aag aga cac ttt      602
Pro Pro Ile Ile Phe His Ala Gly Tyr Ser Leu Lys Lys Arg His Phe
105                                110                                115
ttt caa aac tta gga tct att tta acg tat gcc ttc ttg gga act gcc      650
Phe Gln Asn Leu Gly Ser Ile Leu Thr Tyr Ala Phe Leu Gly Thr Ala
120                                125                                130
atc tcc tgc atc gtc ata ggg taagtgcacat tcggagctca agttgcaggt      701
Ile Ser Cys Ile Val Ile Gly
135                                140
ggctgtgggg tcygtgatct gtgtgagggga tctaacactt ccaggattct tgetggckgg      761
gaaaattgtc ttttttttar tawatcacaw atttgtatgt ttttctwgac ttaattccac      821
ggcttckgam aaatacaagg cttcaaatac aagcaaacta waggattgct ggactttctc      881
tgtgagttct ggacttctga cttaggggaat gtggatcact tgccttgagt tatgtgaagc      941
gcattgcatt cttcttttag tttagtaat sccgatatgc tcaactgcatt cttttttgtc    1001
ttgtattgag agaccttacc tgtatttggc aggagtgcga aagtaactat atgccaagag    1061
ttttctttct aaaggaaagt ttacaagaca gcagtctgaa acagatatgt ccaaatatca    1121
acagagttgc ttaatacagg gatagctttt cagttaatac cctgtagaat gcagactctt    1181
tttttcattg tattttcttg attatgctac tgagccctaa gtcacacggt atatactctg    1241
gcttgcagct catcataaag taaaatgtgg taccaaagg tgaaggcaat ccagcctctg    1301
ataatcccgt ccaatacatt aaagctccac tgcaggaaaa aaaaaa                    1347

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<210> 339

<211> 987

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 124..411

<221> sig_peptide

<222> 124..186

<223> Von Heijne matrix

score 6.30000019073486

seq MVALCCCLWKISG/CE

<221> polyA_signal

<222> 948..953

<221> polyA_site

<222> 971..983

<400> 339

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aagacgctgc ctttagggag agataaaaag cataatgaca ttagctagga aagttaattt      60
tcagttctta ctgaagtgtc gtatgaaact gaaatttcca aggaactgaa tttgtgagc      120
caa atg agc atg caa ttc ttg ttt aag atg gtg gcc tta tgc tgt tgt      168
    Met Ser Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys
      -20              -15              -10

ctc tgg aag atc tcc ggc tgt gag gaa gtc cct cta act tac aac ctg      216
Leu Trp Lys Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu
      -5              1              5              10

ctc aag tgc ctc cta gat aaa gcg cac tgt gta ctc ctg aca cct tgt      264
Leu Lys Cys Leu Leu Asp Lys Ala His Cys Val Leu Leu Thr Pro Cys
              15              20              25

ggg tac atc ttt tcc ttg atc agt cca gaa att ctc aaa ctc act tta      312
Gly Tyr Ile Phe Ser Leu Ile Ser Pro Glu Ile Leu Lys Leu Thr Leu
              30              35              40

atc act ttg cav atc ctc tta ata ctc aaa aat cta cac tta ctg tgg      360
Ile Thr Leu Xaa Ile Leu Leu Ile Leu Lys Asn Leu His Leu Leu Trp
              45              50              55

ctg aca gtt tca agc awa tgt gtt cat cgc agt agt gca aga aaa gaa      408
Leu Thr Val Ser Ser Xaa Cys Val His Arg Ser Ser Ala Arg Lys Glu
              60              65              70

aag tagaagaacc ctgcagagat ttgatggaac ccagcttcta ttcattaaaa      461
Lys
75

ccaatggcaa aatataaagc aaataggagg tgacgaaggt tacaaaaata cgtattgttt      521
atgttttccc tgggtgtgct tgattgtcag gcatcagttc cctgtgccat tcattcccca      581
acacagcatg catcagaaat tttatcaata aatgctttct ctctcaatgt tcaacctatg      641
ctgatagacc attaaataca gtttttgggt tcacagcttg tcatcatcat ttgtctatac      701
ctgtggcaaa gaatatctaa taagatactc tcagcatttt gcacacttaa actaagatgc      761
tgaatgctgt attttacgga ataatacagc acattaaatt tggagactca acaagcatgc      821
tgtgaacatt caacattagg tttaaatttt atttttaaaa gttaataata aaaggatata      881
tgtaagtat tatgaaaccc tgcataact gtaataaaat ggtggatgtg aatggacaat      941
atatgcaata aaatttataa tttgattcya aaaaaaaaaa aamccv      987

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<210> 340

<211> 748

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 372..494

<221> sig_peptide

<222> 372..443

<223> Von Heijne matrix

score 5.30000019073486
seq RILLLHIFYCLLRS/SE

<221> polyA_signal
<222> 708..713

<221> polyA_site
<222> 732..745

<400> 340
 acatgaaatg tgccttggtct gtgatctctt ggtcagatat ctgccttcca ggcgatcctt 60
 tgaggttggtg taattcagct ggccctggct cctggctcct gttactgagc tgggcagtcg 120
 aaccgaaggc agatgagctc aagatcatgc cttgggaagc atggtgctct aggggtgcct 180
 ttttattcct ttcattgtat tatagactgt ttccaagttt atggttagaa atggtaaagt 240
 ggggtctggtg ttttgaggta gaaccagcc tagggcaaga tatgaactgt tcttgaggta 300
 gaaatgtcta cagtcagttg tttcatctag cttgcatctt aaaacacaaa cccttcagtt 360
 gctttcactt a atg cac aca ttt gcc aat gac aga ggg tta tac agg atc 410
 Met His Thr Phe Ala Asn Asp Arg Gly Leu Tyr Arg Ile
 -20 -15
 ctt ctt tta cat ttc tat tgt ctg cta cgc tca tca gag tat att ttg 458
 Leu Leu Leu His Phe Tyr Cys Leu Leu Arg Ser Ser Glu Tyr Ile Leu
 -10 -5 1 5
 ggg tac aag gtt ttg ggg gtt ttt tty ccc att ttg taactgcctt 504
 Gly Tyr Lys Val Leu Gly Val Phe Phe Pro Ile Leu
 10 15
 attgaaaadt aaktgccctt ccattccagg cctcctcata ttgtacttgt ttcctgccaa 564
 atctggggga tcatttgtat ttttaactttg taatctatgg ctctgtactg ttgaaagstc 624
 tcaattctgt ggggtctcct tagtatgtat gtgacttttc atgttgcaat atcacacgat 684
 gggatggccc gacttttgcct ctttaataaat aatctgaatg agtaagaraa aaaaaaaaaa 744
 accc 748

<210> 341
 <211> 1106
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 112..450

<221> sig_peptide
 <222> 112..192
 <223> Von Heijne matrix
 score 7.19999980926514
 seq SLLFFLLLEGGXT/EQ

<221> polyA_signal
 <222> 1053..1058

<221> polyA_site
 <222> 1095..1106

<400> 341
 aagacctcgg aacgagagcg ccccggggag ctcggagcgc gtgcacgcgt ggcavacgga 60
 gaaggcvakk rcnnnnrctt gaaggttctg tcaccttttg cagtggcca a atg aga 117
 Met Arg
 raa aag tgg aaa atg gga ggc atg aaa tac atc ttt tcg ttg ttg ttc 165
 Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe
 -25 -20 -15 -10
 ttt ctt ttg cta gaa gga ggc kaa aca gag caa gtr amn cat tca gag 213

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Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His Ser Glu
-5 1 5
aca tat tgc atg ttt caa gac aag aag tac aga gtg ggt gag aga tgg 261
Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp
10 15 20
cat cct tac ctg gaa cct tat ggg ttg gtt tac tgc gtg aac tgc atc 309
His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile
25 30 35
tgc tca gag aat ggg aat gtg ctt tgc agc cga gtc aga tgt cca aat 357
Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Asn
40 45 50 55
gtt cat tgc ctt tct cct gtg cat att cct cat ctg tgc tgc cct cgc 405
Val His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg
60 65 70
tgc cca gaa gac tcc tta ccc cca gtg aac aat rwg gtg acc agc 450
Cys Pro Glu Asp Ser Leu Pro Pro Val Asn Asn Xaa Val Thr Ser
75 80 85
tagtcttgck agtacaatgg gacaacttac caacatggas agctgttcgt agctgrrggg 510
ctctttcaga atcggaacc cmatcaatgc acccagtga gctgttcgga rggaaacktg 570
tattgtggtc tcaagacttg ccccaaatta acctgtgcct tcccagtcct tgttccarat 630
tcctgctgcc ggggtwtgcag argagatgga caactgtcat gggaacmttc tgatggtgat 690
atcttccggc aacctgcca cagagaagca agacattctt accaccgctc tcactatgat 750
cctccacca gccgacaggc tggaggtctg tcccgtttc ctggggccag aagtcaccgg 810
ggagctctta tggattccca gcaagcatca ggaaccattg tgcaaattgt catcaataac 870
aaacacaagc atggacaagt gtgtgtttcc aatggaaaga cctattctca tggcgagtcc 930
tggcacccaa acctccgggc atttggcatt gtggagtgtg tgctatgtac ttgtaatgtc 990
accaagcaag agtctaagaa aatccactgc cccaatcgat acccctgcaa gtatcctcaa 1050
aaaatagacg gaaaatgctg caaggtgtgt ccaggtaaaa aagcaaaaaa aaaaaa 1106

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<210> 342

<211> 1191

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 117..866

<221> sig_peptide

<222> 117..170

<223> Von Heijne matrix

score 10.6999998092651

seq LILLALATGLVGG/ET

<221> polyA_signal

<222> 1159..1164

<221> polyA_site

<222> 1178..1190

<400> 342

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aaaaccagc ctacctgctg tagctgccgc cactgccgtc tccgccgcca ctggwccccc 60
agagcbnmag cccagagcc taggaacctg gggcccgtc ctccccctc caggcc atg 119
Met
agg att ctg cag tta atc ctg ctt gct ctg gca aca ggg ctt gta ggg 167
Arg Ile Leu Gln Leu Ile Leu Ala Leu Ala Thr Gly Leu Val Gly
-15 -10 -5
gga gag acc agg atc atc aag ggg ttc gag tgc aag cct cac tcc cag 215
Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln
1 5 10 15

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ccc tgg cag gca gcc ctg ttc gag aag acg cgg cta ctc tgt ggg gcg      263
Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala
      20                      25                      30
acg ctc atc gcc ccc aga tgg ctc ctg aca gca gcc cac tgc ctc aag      311
Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys
      35                      40                      45
ccc cgc tac ata ktt cac ctg ggg cag cac aac ctc cag aag gag gag      359
Pro Arg Tyr Ile Xaa His Leu Gly Gln His Asn Leu Gln Lys Glu Glu
      50                      55                      60
ggc tgt gag car acc cgg aca gcc act gag tcc ttc ccc cac ccc ggc      407
Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly
      65                      70                      75
ttc aac aac agc ctc ccc aac aaa gac cam mgc aat gac atc atg ctg      455
Phe Asn Asn Ser Leu Pro Asn Lys Asp Xaa Xaa Asn Asp Ile Met Leu
      80                      85                      90                      95
gtg aak atg gma tgc cca gtc tcc atc acc tgg gct gtg cga ccc ctc      503
Val Xaa Met Xaa Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro Leu
      100                      105                      110
acc ctc tcc tca cgc tgt gtc act gct ggc acc agc tgc ctc att tcc      551
Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile Ser
      115                      120                      125
ggc tgg ggc agc acg tcc agc ccc cag tta cgc ctg cct cac acc ttg      599
Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu
      130                      135                      140
cga tgc gcc aac atc acc atc att gag cac cag aag tgt gag aac gcc      647
Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala
      145                      150                      155
tac ccc ggc aac atc aca gac acc atg gtg tgt gcc agc gtg cag gaa      695
Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu
      160                      165                      170                      175
ggg ggc aag gac tcc tgc cag ggt gac tcc ggg ggc cct ctg gtc tgt      743
Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
      180                      185                      190
aac cag tct ctt caa ggc att atc tcc tgg ggc cag gat ccg tgt gcg      791
Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
      195                      200                      205
atc acc cga aag cct ggt gtc tac acg aaa gtc tgc aaa tat gtg gac      839
Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val Asp
      210                      215                      220
tgg atc cag gag acg atg aag aac aat tagactggac ccacccacca      886
Trp Ile Gln Glu Thr Met Lys Asn Asn
      225                      230
cagcccatca ccctccattt ccacttggtg tttggttctt gttcactctg ttaataagaa      946
accctaagcc aagaccctct acgaacattc tttgggcctc ctggactaca ggagatgctg      1006
tcacttaata atcaacctgg ggttcgaaat cagtgaagacc tggattcaaa ttctgccttg      1066
aaatattgtg actctgggaa tgacaacacc tggtttgctt tctgttgat cccagcccc      1126
aaakwcagct cctggccata tatcaaggtt tcaataaata tttgctaaat gaawaaaaaa      1186
aaaac                                          1191

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<210> 343

<211> 1070

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 13..465

<221> sig_peptide

<222> 13..75

<223> Von Heijne matrix
score 3.90000009536743
seq PVAVTAAVAPVLS/IN

<221> polyA_signal

<222> 1035..1040

<221> polyA_site

<222> 1060..1070

<400> 343

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agagtcggga aa atg gct gcg agt acc tcc atg gtc ccg gtg gct gtg acg      51
      Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr
      -20              -15              -10
gcg gca gtg gcg cct gtc ctg tcc ata aac agc gat ttc tca gat ttg      99
Ala Ala Val Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu
      -5              1              5
cgg gaa att aaa aag caa ctg ctg ctt att gcg ggc ctt acc cgg gag      147
Arg Glu Ile Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu
      10              15              20
cgg ggc cta cta cac agt agc aaa tgg tgg gcg gag ttg gct ttc tct      195
Arg Gly Leu Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser
      25              30              35              40
ctc cct gca ttg cct ctg gcc gag ctg caa ccg cct ccg cct att aca      243
Leu Pro Ala Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr
      45              50              55
gag gaa gat gcc cag gat atg gat gcc tat acc ctg gcc aag gcc tac      291
Glu Glu Asp Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr
      60              65              70
ttt gac gtt aaa gag tat gat cgg gca gca cat ttc ctg cat ggc tgc      339
Phe Asp Val Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys
      75              80              85
aat gca aga aaa gcc tat ttt ctg tat atg tat tcc aga tat ctg gtg      387
Asn Ala Arg Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val
      90              95              100
agg gcc att tta aaa tgt cat tct gcc ttt agt gaa aca tcc ata ttt      435
Arg Ala Ile Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe
      105              110              115              120
aga acc aat gga aaa gtt aaa tct ttt aaa tagcttagca gtgggccact      485
Arg Thr Asn Gly Lys Val Lys Ser Phe Lys
      125              130
gaatgaatgt actttataca tagcaataat aaaaaaaga tatcataaat aaagttaaaa      545
aggatggtaa aaaaaaaaaat attcttagga atgactaaca ggataagtaa caacctgatt      605
atattattac tttagggttat ataagggtct tcatgcctgt gaattaatat tattgtgtaa      665
gaattaagtt aaaaagcctg ggctgacttt taaatttata aattcattta tcatgtttat      725
agtatattta ttgtttttct ttcattggcta ttaaaaagta tgactgtaaa ggacaatgca      785
agtaaaccac ctaataactg tattgaataa taagtacaat ttattatttt actttgaaac      845
attatgaatt tactttccta ctttttctta gttgttatct atataaattg attaaaaaaa      905
cattttatgt acttctcatt tcctagtaca gggtgagtat cccttatttg aagtgtctgg      965
gaccaaagt gtttcagatt tcagattttt ttcagatttt ggtatatttg cattatactt      1025
actgggtgaa ataaaaaatg ctgcagtgag tgtcaaaaaa aaaaaa      1070

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<210> 344

<211> 1213

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 2..718

<221> sig_peptide

<222> 2..76

<223> Von Heijne matrix

score 3.90000009536743

seq RVGLLLGGGGVYG/SR

<221> polyA_signal

<222> 1170..1175

<221> polyA_site

<222> 1203..1213

<400> 344

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a atg ccc cgg aag cgg aag tgc gat ctt cgg gct gtc aga gtt ggt ctg      49
Met Pro Arg Lys Arg Cys Asp Leu Arg Ala Val Arg Val Gly Leu
-25 -20 -15 -10
tta ctc ggt ggt ggc gga gtc tac gga agc cgt ttt cgc ttc act ttt      97
Leu Leu Gly Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
-5 1 5
cct ggc tgt aga gcg ctt tcc ccc tgg cgg gtg aga vtg cag aga cga      145
Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
10 15 20
agg tgc gag atg agc act atg ttc gcg gac act ctc ctc atc gtt ttt      193
Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
25 30 35
atc tct gtg tgc acg gct ctg ctc gca gag ggc ata acc tgg gtc ctg      241
Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
40 45 50 55
gtt tac agg aca gac aag tac aag aga ctg aag gca gaa gtg gaa aaa      289
Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
60 65 70
cag agt aaa aaa ttg gaa aag aag aag gaa aca ata aca gag tca gct      337
Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala
75 80 85
ggg cga caa cag aaa aar aaa ata gag aga cdd kaa kas amc ctg arg      385
Gly Arg Gln Gln Lys Lys Lys Ile Glu Arg Xaa Xaa Xaa Xaa Leu Xaa
90 95 100
aat aac aac aga gat cta tca atg gtt cga atg aaa tcc atg ttt gct      433
Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala
105 110 115
att ggc ttt tgt ttt act gcc cta atg gga atg ttc aat tcc ata ttt      481
Ile Gly Phe Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser Ile Phe
120 125 130 135
gat ggt aga gtg gtg gca aag ctt cct ttt acc cct ctt tct tas rtc      529
Asp Gly Arg Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser Xaa Xaa
140 145 150
sra gga ctg tct cat cga aat ctg ctg gga gat gac acc aca gac tgt      577
Xaa Gly Leu Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr Asp Cys
155 160 165
tcc ttc att ttc ctg taw att ctc tgt act atg tcg att cga cag aac      625
Ser Phe Ile Phe Leu Xaa Ile Leu Cys Thr Met Ser Ile Arg Gln Asn
170 175 180
att cag aag att ctc ggc ctt gcc cct tca cga gcc gcc acc aag cag      673
Ile Gln Lys Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr Lys Gln
185 190 195
gca ggt gga ttt ctt ggc cca cca cct cct tct ggg aag ttc tct      718
Ala Gly Gly Phe Leu Gly Pro Pro Pro Pro Gly Lys Phe Ser
200 205 210
tgaactcaag aactctttat tttctakcat tctttctaga cacacacaca tcagactggc      778
aactgttttg tascaagagc cataggtagc cttackactt gggcctcttt ctagtgttga      838
attatttcta agccttttgg gtatkattag agtgaaaatg gcagccagca aacttgatag      898

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ccc cga gca cac gtg gaa tcg agc ara ctg aaa stc wtg cat ttt gtg      592
Pro Arg Ala His Val Glu Ser Ser Xaa Leu Lys Xaa Xaa His Phe Val
          65          70          75
gca agg gtt cgt aac cga tgc tct aaa gac tgg cct tgt aat tat gac      640
Ala Arg Val Arg Asn Arg Cys Ser Lys Asp Trp Pro Cys Asn Tyr Asp
          80          85          90
tgg gat tcg gac gat gat gca gag gtt gag gct atc ctc aat tca ggt      688
Trp Asp Ser Asp Asp Asp Ala Glu Val Glu Ala Ile Leu Asn Ser Gly
          95          100          105
gct arg ggt tat tcc gcc cct taagtaratc tgaggcagac ccttggggggt      739
Ala Xaa Gly Tyr Ser Ala Pro
110          115
gtaaaagaga gtcacaggtta ccccaaggag tagatgccag ggtcctaagt tgaaaatgmt      799
gtcgattggg ggcggggggac actgtatttg atatttgtga tcagtgatca ttgttcaact      859
gcgaaataga gtgtttgctt ttgataatgg aaaattgtat tcgtttttaa attccgtttg      919
ttgagaataa caatatgttt aaaaatataa ttgaacaaat tttaaaaaaa aaaamcccy      978

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<210> 346
 <211> 810
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..320

<221> sig_peptide
 <222> 63..179
 <223> Von Heijne matrix
 score 3.90000009536743
 seq VLAIGLLHIVLLS/IP

<221> polyA_signal
 <222> 771..776

<221> polyA_site
 <222> 799..810

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<400> 346
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gg atg aat gtk ggc aca gcg cac ags dag gtg aac ccc aac acg cgg      107
Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg
          -35          -30          -25
gtk atg aac agc cgt ggc atc tgg ctc tcc tac gtg ctg gcc atc ggt      155
Val Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly
          -20          -15          -10
ctc ctc cac atc gtg ctg ctg agc atc ccg ttt gtk agt gtc cct gtc      203
Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val
          -5          1          5
gtc tgg acc ctc acc aac ctc att cac aac atg ggc atg tat atc ttc      251
Val Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe
          10          15          20
ctg cac acg gtg aag ggg aca ccc ttt gag acc ccg gac cag ggc aag      299
Leu His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys
          25          30          35          40
gcg agg ctg cta acc cac tgg tgagcagatg gattatgggg tccagttcac      350
Ala Arg Leu Leu Thr His Trp
          45
ggcctctcgg aaktctctga ccatcacacc catcgtgctg tacttctctca ccagcttcta      410
cactaaktac raccaaattc attttgtgct caacaccgtg tccctgatra gcgtgcttat      470

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ccccaagctg	ccccagctcc	acggaktccg	gatttttggga	atcaataakt	actgaaaktg	530
cascccccttc	ccctgcccag	ggtggcaggg	gaggggtagg	gtaaaaggca	tktgctgcaa	590
chctgaaaac	araaaraara	rscctctgga	cactgccara	ratgggggtt	gagcctctgg	650
cctaatttcc	cccctcgctt	ccccagtag	ccaacttggga	gtagcttgta	ytgggggttg	710
ggtaggcccc	ctgggctctg	accttttctg	aattttttga	tcttttcctt	ttgctttttg	770
aatararact	ccatggagtt	ggtcatggaa	aaaaaaaaaa			810

<210> 347
 <211> 771
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 299..418

<221> sig_peptide
 <222> 299..379
 <223> Von Heijne matrix
 score 3.59999990463257
 seq LTLLLITSPSPSL/LF

<221> polyA_signal
 <222> 739..744

<221> polyA_site
 <222> 762..771

<400> 347	
accttgggct ccaaattcta gctcataaag atgcaagtkt tgcaatttcc tataaatggt	60
taagaaaaga gcaagctgtc cagagagtga gaagtttgaa aagagagggt cataagagag	120
aatgatgtc catttgagcc ccaccacgga ggttatgtgg tcccaaaagg aatgatggcc	180
aagcaattaa tttttcctcc tagttcttag cttgcttctg cattgattgg ctttacacaa	240
ctggcattta gtctgcatta cacaaataga cactaattta tttggaacaa gcagcaaa	298
atg aga act tta ttt ggt gca gtc agg gct cca ttt agt tcc ctc act	346
Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr	
-25 -20 -15	
ctg ctt cta atc acc cct tct ccc agc cct ctt cta ttt gat aga ggt	394
Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly	
-10 -5 1 5	
ctg tcc ctc aga tca gca atg tct tagccccctct cctctcttcc attccttcct	448
Leu Ser Leu Arg Ser Ala Met Ser	
10	
gttggtactc atttcttcta acttttaata aacatttagg tataatacat tacagtaagt	508
gctattttaga tacaaactta aaacatacta tatattttta ggatctaaga atcctttara	568
rrrggcacat gactgaagta cctcagctgc gcagcctgta accagttttt ttaatgtaaa	628
agtaaraatg ccagccttaa cctabccctg carataaaag ctaactttta ttaataccag	688
ccctgaataa tggcactaat ccacactctt ccttaragtg atgctggaaa aataaaatca	748
ggggcttcag attaaaaaaa aaa	771

<210> 348
 <211> 409
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 186..380

<221> sig_peptide
 <222> 186..233
 <223> Von Heijne matrix
 score 4
 seq FFLFLSFVLMYDG/LR

<221> polyA_signal
 <222> 383..388

<221> polyA_site
 <222> 396..409

<400> 348
 ataaaagaag cagcaaatag aatttccac aaagtaagtt gactctaaat cttaagtatt 60
 acctagtttt ttaaagggtt gaatataata atgcagtatt tgcagtataa aaaggaagga 120
 atttgtagag aatcattttg gtgctcaagt ctcttagcag tgccttattg cctcatagca 180
 agaag atg ctg ggg ttt ttt ttg ttt ttg tcc ttt gta tta atg tat gat 230
 Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp
 -15 -10 -5
 ggt ttg cgc ctt ttt ggc att ctt tca aca tgt cgt gta cat cac acc 278
 Gly Ieu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr
 1 5 10 15
 atg aat cag ttc cta att gat ata tct agc ttt acc tcc cga gtt aaa 326
 Met Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Lys
 20 25 30
 aaa aaa atc ttt tta ttt tat gcc ttc awa ggt tgc ycg ttt car agt 374
 Lys Lys Ile Phe Leu Phe Tyr Ala Phe Xaa Gly Cys Xaa Phe Gln Ser
 35 40 45
 gcc aca taaataaaat gtttaacaaa aaaaaaaaaa 409
 Ala Thr

<210> 349
 <211> 613
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..458

<221> sig_peptide
 <222> 69..233
 <223> Von Heijne matrix
 score 4
 seq AALCGISLSQLFP/EP

<221> polyA_signal
 <222> 564..569

<221> polyA_site
 <222> 602..613

<400> 349
 aagaacctga gcagcctgtc ttcagacaga gagaggccca cggctgtttc ttgaaaytgg 60
 cgctggga atg gcc atg tgg aac agg cca tgb bag ang ctg cct cag cag 110
 Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln
 -55 -50 -45
 cct cts sta gct gag ccc act gca gag ggg gag cca cac ctg ccc acg 158
 Pro Leu Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr

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-40          -35          -30
ggc cgg gas byg act gag gcc aac cgc ttc gcc tat gct gcc ctc tgt      206
Gly Arg Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys
-25          -20          -15          -10
ggc atc tcc ctg tcc cag tta ttt cct gaa ccc gaa cac agc tcc ttc      254
Gly Ile Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe
          -5          1          5
tgc aca gag ttc atg gca ggc ctg gtg ckm tgg ctg gag ttg tct gaa      302
Cys Thr Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu
          10          15          20
gct gtc ttg cca acc atg act gct ttt gcg agc ggc ctg gga ggt gaa      350
Ala Val Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu
          25          30          35
gga sca vma tgt gtt tgt tca aat ttt act gaa gga ccc cat ctt gaa      398
Gly Xaa Xaa Cys Val Cys Ser Asn Phe Thr Glu Gly Pro His Leu Glu
          40          45          50          55
gga cga ccc gac ggt gat cac tca gga cct tct gag ctt ctc act caa      446
Gly Arg Pro Asp Gly Asp His Ser Gly Pro Ser Glu Leu Leu Thr Gln
          60          65          70
gga tgg gca cta tgacscgccg gccagagtc tggtttgcca catgacctcc      498
Gly Trp Ala Leu
          75
ctgctccaag tgccttgga ggagctggat gtccttgaaa agatgttcct ggagagcctg      558
aaggaaatca aagaagagga atctgaaatg gccgaggcat cccraaaaaa aaaaa      613

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<210> 350
 <211> 986
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..638

<221> sig_peptide
 <222> 12..263
 <223> Von Heijne matrix
 score 4.19999980926514
 seq ITMLQMLALLGYG/LF

<221> polyA_signal
 <222> 951..956

<221> polyA_site
 <222> 975..985

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<400> 350
accctatcaa g atg gtc aac ttc ccc cag aaa att gca ggt gaa ctc tat      50
          Met Val Asn Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr
          -80          -75
gga cct ctc atg ctg gtc ttc act ctg gtt gct atc cta ctc cat ggg      98
Gly Pro Leu Met Leu Val Phe Thr Leu Val Ala Ile Leu Leu His Gly
          -70          -65          -60
atg aag acg tct gac act att atc cgg gag ggc acc ctg atg ggc aca      146
Met Lys Thr Ser Asp Thr Ile Ile Arg Glu Gly Thr Leu Met Gly Thr
          -55          -50          -45          -40
gcc att ggc acc tgc ttc ggc tac tgg ctg gga gtc tca tcc ttc att      194
Ala Ile Gly Thr Cys Phe Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile
          -35          -30          -25
tac ttc ctt gcc tac ctg tgc aac gcc cag atc acc atg ctg cag atg      242

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Tyr Phe Leu Ala Tyr Leu Cys Asn Ala Gln Ile Thr Met Leu Gln Met
      -20              -15              -10
ttg gca ctg ctg ggc tat ggc ctc ttt ggg cat tgc att gtc ctg ttc      290
Leu Ala Leu Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe
      -5              1              5
atc acc tat aat atc cac ctc cgc gcc ctc ttc tac ctc ttc tgg ctg      338
Ile Thr Tyr Asn Ile His Leu Arg Ala Leu Phe Tyr Leu Phe Trp Leu
      10              15              20              25
ttg gtg ggt gga ctg tcc aca ctg cgc atg gta gca gtg ttg gtg tct      386
Leu Val Gly Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser
      30              35              40
cgg acc gtg ggc ccc aca cad cgg mtg ctc ctc tgt ggc acc ctg gct      434
Arg Thr Val Gly Pro Thr Xaa Arg Xaa Leu Leu Cys Gly Thr Leu Ala
      45              50              55
gcc cta cac atg ctc ttc ctg ctc tat ctg cat ttt gcc tac cac aaa      482
Ala Leu His Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys
      60              65              70
dtg gta dag ggg atc ctg gac aca ctg gag ggc ccc aac atc ccg ccc      530
Xaa Val Xaa Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro
      75              80              85
atc cag agg gtc ccc aga gac atc cct gcc atg ctc cct gct gct cgg      578
Ile Gln Arg Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg
      90              95              100              105
ctt ccc acc acc gtc ctc aac gcc aca gcc aaa gct gtt gcg gtg acc      626
Leu Pro Thr Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr
      110              115              120
ctg cag tca cac tgacccacc tgaaattctt ggccagtcct ctttcccgca      678
Leu Gln Ser His
      125
gctgcagaga ggargaasac tattaaagga cagtcctgat gacatgtttc gtagatgggg      738
tttgacagctg ccactgagct gtagctgcgt aagtacctcc ttgatgcctg tcggcacttc      798
tgaaaggcac aaggccaaga actcctggcc aggactgcaa ggctctgcag ccaatgcaga      858
aaatgggtca gctcctttga gaacccctcc ccacctaccc cttccttcct ctttatctct      918
cccacattgt cttgctaaat atagacttgg taattaaaat gttgattgaa gtctggaaaa      978
aaaaaaat      986

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<210> 351

<211> 1447

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 282..389

<221> sig_peptide

<222> 282..332

<223> Von Heijne matrix

score 3.5

seq RWWCFHLQAEASA/HP

<221> polyA_signal

<222> 1413..1418

<221> polyA_site

<222> 1437..1447

<400> 351

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ataataatat ctaaaaagct aaatttttaa taccagcttt acataaatga ttgtkgactc      60
tggtctgtkt ctgacacctt tccagaaaaa agtcaattgt tcaggtacac caaaggaggaa      120

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gaagagctgt ggaggccacc ctctacaaag ctttatagaa cttctggatc taactcacaa 180
acaagcttcc agaagagact agagacctta ggccaggaga tgaaggagtt cagtagcaaa 240
gtcacacctg tccaattccc tgagctttgc tcactcagct a atg gga tgg caa agg 296
                                     Met Gly Trp Gln Arg
                                     -15
tgg tgg tgc ttt cat ctt cag gca gaa gcc tct gcc cat ccc cct caa 344
Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser Ala His Pro Pro Gln
      -10      -5      1
ggg ctg cag gcc caa ttc tca tgc tgc cct tgg gtg ggc atc tgt 389
Gly Leu Gln Ala Gln Phe Ser Cys Cys Pro Trp Val Gly Ile Cys
5      10      15
taacaaadga aaacgtctgg gtggcggcag casctttgct ctgagtgcct acaaagctaa 449
tgcttgggtgc tagaaacatc atcattatta aacttcagaa aagcagcagc catgttcagt 509
caggctcatg ctgcctcact gcttaagtgc ctgcaggagc cgcctgccaa rctccccttc 569
ctacacctgg cacactgggg tctgcacaag gctttgtcaa ccaaaracag cttccccww 629
ttgattgcct gtagactttg gagccaaraa acactctgtg tgactctaca cacacttcag 689
gtggtttgtg cttcaaagtc attgatgcaa cttgaaagga aacagttaa tgggtggaaat 749
gaactaccat ttataacttc tgttttttta ttgagaaaat gattcacgaa kkccaaatca 809
gattgccagg aagaaatagg acgtgacggt actgggccct gtgattctcc cagcccttgc 869
agtcgcctag gtgagaggaa aagctcttta ctccgccccc tggcagggac ttctgggtta 929
tggaagaaac cagagatggg aatgaggaaa atatgaacta cagcagaagc ccctgggcag 989
ctgtgatgga gcccctgaca ttactcttct tgcactctgc ctgccttctt tccctctgcg 1049
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gcatgcaagc cctgctgtgt ggctgtcggt tacatttggg aggtgtcctg tatgtctgta 1169
cggtggggac tgcctgtatt tggaagattt aaaaacctag catcctgttc tcacctcta 1229
agctgcattg agaaatgact cgtctctgta tttgtattaa gccttaaac ttttcttaag 1289
tgcattcggg gccaacattt tttagagctg taccaaaaca aaaagcctgt actcacatca 1349
camtgtcatt ttgataggag cgttttgta tttttacaag gcagaatggg gtgtaacagt 1409
tgaattaaac tttagcaatca cgtgctcaaa aaaaaaaaa 1447

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<210> 352
 <211> 1641
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 208..339

<221> sig_peptide
 <222> 208..294
 <223> Von Heijne matrix
 score 5.59999990463257
 seq LFLQLLVSHIVC/AT

<221> polyA_site
 <222> 1631..1641

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<400> 352
agaaccgtga tgggaagatg gacaaggaag agaccaaaga ctggatcctt ccctcagact 60
atgatcatgc agaggcagaa gccaggcacc tgggtctatga atcagaccaa aacaaggatg 120
gcaagcttac caaggaggag atcgttgaca agtatgactt atttgttggc agccaggcca 180
cagattttgg ggaggcctta gtacggc atg atg agt tct gag cta cgg agg aac 234
                                     Met Met Ser Ser Glu Leu Arg Arg Asn
                                     -25
cct cat ttc ctc aaa agt aat tta ttt tta cag ctt ctg gtt tca cat 282
Pro His Phe Leu Lys Ser Asn Leu Phe Leu Gln Leu Leu Val Ser His
-20      -15      -10      -5
gaa att gtt tgc gct act gag act gtt act aca aac ttt tta aga cat 330
Glu Ile Val Cys Ala Thr Glu Thr Val Thr Thr Asn Phe Leu Arg His

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	1	5	10	
gaa aag gcg taatgaaaac catcccgctcc ccattcctccc tcctctctga				379
Glu Lys Ala				
15				
gggactggag ggaagccgtg cttctgagga acaactctaa ttagtacact tgtgtttgta				439
ratttacacw wtgtattatg tattaacatg gcgtgtttat ttttgtattt ttctctgggt				499
gggagtatka tatgaaggat caaratctc aactcacaca tataracaaa cattasctct				559
ttactctttc tcaaccctt wtatgatttt aataattctc acttaactaa ttttgtaagc				619
ctgagatcaa taagaaatgt tcaggagaga ggaaagaaaa aaaatatatg ctccacaatt				679
tatatttaga gagagaacac ttagtcttgc ctgtcaaaaa gtccaacatt tcataggtag				739
taggggccac atattacatt cagttgctat aggtccagca actgaacctg ccattacctg				799
ggcaaggaaa gatccctttg ctctaggaaa gcttggccca aattgatttt cttctttttc				859
cccctgtagg actgactgtt ggctaatttt gtcaagcaca gctgtggtgg gaagagttag				919
ggccagtgtc ttgaaaatca atcaagtagt gaatgtgac tctttgcara gctatagata				979
gaaacagctg gaaaactaaa ggaaaaatcac aagtgttttc ggggcataca ttttttttct				1039
gggtgtgcat ctgttgaaat gctcaagact taattatttg ccttttgaaa tcaactgtaa				1099
tgcccccac cggttcctct tcttccarg tgtgccaagg aattaatctt ggtttcaacta				1159
caattaaaat tcaactcctt ccaatcatgt cattgaaagt gcctttaacg aaagaaatgg				1219
tcaactgaatg ggaattctct taagaaaccc tgagattaaa aaaagactat ttggataact				1279
tataggaaag cctagaacct ccagtagag tggggatttt tttcttcttc cctttctctt				1339
ttggacaata gttaaattag cagtattagt tatgagtttg gttgcagtgt tcttatcttg				1399
tgggctgatt tccaaaaacc acatgctgct gaatttacca gggatcctca tacctcacia				1459
tgcaaaccac ttactaccag gcctttttct gtgtccactg gagagcttga gctcacactc				1519
aaagatcaga ggacctacag agagggtctt ttggtttgag gaccatggct tacctttcct				1579
gcctttgacc catcacacc catttctctc tctttccctc tccccgctgc caaaaaaaaa				1639
aa				1641

<210> 353
 <211> 884
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..557

<221> sig_peptide
 <222> 69..224
 <223> Von Heijne matrix
 score 4.69999980926514
 seq LGLALGRLEGGSA/RH

<221> polyA_signal
 <222> 849..854

<221> polyA_site
 <222> 870..883

<400> 353	
attggctccg gatcgtgcgt gaggcggctt cgtgggcagc gagagtcaca gacaagacag	60
caagcagg atg gag cac tac cgg aaa gct ggc tct gta gag ctc cca gcg	110
Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala	
-50 -45 -40	
cct tcc cca atg ccc cag cta cct cct gat acc ctt gag atg cgg gtc	158
Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val	
-35 -30 -25	
cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct ctg ggt cgg	206
Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg	
-20 -15 -10	
ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt tct ggc agg	254

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Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg
-5          1          5          10
gct gca gga aag gct gtc agc tgc gct gag att gtc aag cgg cgg gtc      302
Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val
          15          20          25
ccg ggc ctg cac cag ctc acc aag cta ckt ttc ctt caa act gag gac      350
Pro Gly Leu His Gln Leu Thr Lys Leu Xaa Phe Leu Gln Thr Glu Asp
          30          35          40
agc tgg gtc cca scc tca cct gac aca ggg cta rac ccc ctc aca gtg      398
Ser Trp Val Pro Xaa Ser Pro Asp Thr Gly Leu Xaa Pro Leu Thr Val
          45          50          55
cgc cgc cat gtg cct gca ktg tgg gtg ctg ctc asc cgg gac ccc ctg      446
Arg Arg His Val Pro Ala Xaa Trp Val Leu Leu Xaa Arg Asp Pro Leu
          60          65          70
gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc cct ggc ctg      494
Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu
          75          80          85          90
ggt tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cra aaa agg gct      542
Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Xaa Lys Arg Ala
          95          100          105
cra rac acc cga tgc tgaaaacctg ctgascacgc ctgttctccg ggcctraatg      597
Xaa Xaa Thr Arg Ser
          110
tctgggggtgc ttgtgccttt tctranaagc gttgtgaskg ctcaacatcc ccatcaaggt      657
ttgagtcacac aaaagtggac ctccctatca tgcttccctt tccctctagc atgtgggaag      717
ggactgctgt gaagaatgac agatgtgggg cctctgccaa gttctgcatt gctaaataag      777
ggcttctctt gccttctacc tacagtgcac ttgaactgcc ttctgaaaga ggtccakgga      837
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<210> 354

<211> 729

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 134..325

<221> sig_peptide

<222> 134..274

<223> Von Heijne matrix

score 5.90000009536743

seq TWLGLLSFQNLHC/FP

<221> polyA_site

<222> 718..729

<400> 354

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tgtaatgcaa gtccctaac tccctggttg ctaacattaa ctcccttaag taataatcaa      120
tgaaagavat tct atg cat ggt ttt gaa ata ata tcc ttg aaa gag gaa      169
          Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu
          -45          -40
tca cca tta gga aag gtg agt cag ggt cct ttg ttt aat gtg act agt      217
Ser Pro Leu Gly Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser
-35          -30          -25          -20
ggc tca tca tca cca gtg acc tgg ttg ggc cta ctc tcc ttc cag aac      265
Gly Ser Ser Ser Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn
          -15          -10          -5
ctg cat tgc ttc cca gac ctc ccc act gag atg cct cta ara gcc aaa      313

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Leu His Cys Phe Pro Asp Leu Pro Thr Glu Met Pro Leu Xaa Ala Lys

1 5 10
gga ktc aac act tgagcctagg gtgggctaca acaaaaratt ctaatttacc 365
Gly Xaa Asn Thr
15
ttgcttcac taggtccagg ccccaaktag cttgctgaag gaacttaaaa agtagctgtt 425
atttattgta ttgtataasc taaaaacatt tatttttgtt gaatcraaac aattccatgt 485
ascaatcttt tttctgttca cgggtgttgt gataaaacct taaattccgc aagcatcagt 545
tttttgaaaa aatgggaatt gaccggatag wwacaggcaa agwtataaat agctacaaca 605
tcatttaact tttataaaca tgcttctct ctattgaara catctgatat ttttgctgga 665
aagttggatc tatcctcagt aactctgcca tgaattcttg tttcckgggt ccaaaaaaaa 725
aaaa 729

<210> 355

<211> 1013

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 78..731

<221> sig_peptide

<222> 78..227

<223> Von Heijne matrix

score 5.09999990463257

seq RTALILAVCCGSA/SI

<221> polyA_site

<222> 1002..1013

<400> 355

agtttccaag ggaaggagca gcggtgtggga aagcacagaa gagtgagaag gaagcgacta 60
aattttattt actttct atg cat cat ggc ctc aca cca ctg tta ctt ggt 110
Met His His Gly Leu Thr Pro Leu Leu Leu Gly
-50 -45 -40
gta cat gag caa aaa cag caa gtg gtg aaa ttt tta atc aag aaa aaa 158
Val His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys
-35 -30 -25
gca aat tta aat gca ctg gat aga tat gga aga act gct ctc ata ctt 206
Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu
-20 -15 -10
gct gta tgt tgt gga tcg gca agt ata gtc agc ctt cta ctt gag caa 254
Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln
-5 1 5
aac att gat gta tct tct caa gat cta tct gga cag acg gcc aaa aag 302
Asn Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Lys Lys
10 15 20 25
tat gct gtt tct agt cgt cat aat gta att tgc cag tta ctt tct gac 350
Tyr Ala Val Ser Ser Arg His Asn Val Ile Cys Gln Leu Leu Ser Asp
30 35 40
tac aaa raa aaa cag atr cta aaa gtc tct tct gaa aac agc aat cca 398
Tyr Lys Xaa Lys Gln Xaa Leu Lys Val Ser Ser Glu Asn Ser Asn Pro
45 50 55
raa caa gac tta aag ctg aca tca gag gaa gag tca caa agg ctt aaa 446
Xaa Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Lys
60 65 70
gga agt gaa aat agc cag cca gag gaa atg tct caa gaa cca gaa ata 494
Gly Ser Glu Asn Ser Gln Pro Glu Glu Met Ser Gln Glu Pro Glu Ile
75 80 85

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aat arg ggt ggt gat aga aag gtt gaa raa raa atg aar aag cac gga      542
Asn Xaa Gly Gly Asp Arg Lys Val Glu Xaa Xaa Met Lys Lys His Gly
90          95          100          105
agt wct cat atg gga ttc cca raa aac ctg mct aac ggt gcc act gct      590
Ser Xaa His Met Gly Phe Pro Xaa Asn Leu Xaa Asn Gly Ala Thr Ala
          110          115          120
gac aat ggt gat gat gga tta att ccm cca rgg aaa asc ara aca cct      638
Asp Asn Gly Asp Asp Gly Leu Ile Pro Pro Xaa Lys Xaa Xaa Thr Pro
          125          130          135
gaa agc cas caa ttt cct gac act gag aat gaa cag tat cac agg gac      686
Glu Ser Xaa Gln Phe Pro Asp Thr Glu Asn Glu Gln Tyr His Arg Asp
          140          145          150
ttt tct ggc cat ccc mac ttt ccc acd acc ctt ccc atc aaa cag      731
Phe Ser Gly His Pro Xaa Phe Pro Thr Leu Pro Ile Lys Gln
          155          160          165
tgatgaacaa aatgatactc hsaagcmmct ttctgaagam caraacactg gaatattaca      791
agatgagatt ctgattcatg aagaaaagca gatagaagtg gctgaaaatg aattctgagc      851
tttctcttag ttataaaaa gaaaaagacc tcttgcataa aaatagtacg ttgcaggaag      911
aaattgtcat gctaaractg gaactagack taatgaaaca tcagagccag ctaaraaaaa      971
araaatattt ggaggaaatt gaaagtgtgg aaaaaaaaaa aa      1013

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<210> 356

<211> 973

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 46..693

<221> sig_peptide

<222> 46..90

<223> Von Heijne matrix

score 7.59999990463257

seq CVLVLAAGAVA/VF

<221> polyA_signal

<222> 937..942

<221> polyA_site

<222> 962..973

<400> 356

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aagcggctgg tccccggaag ttggacgcat gcgcggtttc tctgc atg gtg tgc gtt      57
                                   Met Val Cys Val
                                   -15
ctc gtt cta gct gcg gcc gca gga gct gtg gcg gtt ttc cta atc ctg      105
Leu Val Leu Ala Ala Ala Ala Gly Ala Val Ala Val Phe Leu Ile Leu
-10          -5          1          5
cga ata tgg gta gtg ctt cgt tcc atg gac gtt acg ccc cgg gag tct      153
Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr Pro Arg Glu Ser
          10          15          20
ctc agt atc ttg gta gtg gct ggg tcc ggt ggg cat acc act gag atc      201
Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His Thr Thr Glu Ile
          25          30          35
ctg agg ctg ctt ggg agc ttg tcc aat gcc tac tca cct aga cat tat      249
Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser Pro Arg His Tyr
          40          45          50
gtc att gct gac act gat gaa atg agt gcc aat aaa ata aat tct ttt      297
Val Ile Ala Asp Thr Asp Glu Met Ser Ala Asn Lys Ile Asn Ser Phe

```

55	60	65	
gaa cta rat cga gsk gat aga rac cct agt aac atg twt acc aaa tac			345
Glu Leu Xaa Arg Xaa Asp Arg Xaa Pro Ser Asn Met Xaa Thr Lys Tyr			
70	75	80	85
tac att cac cga att cca ara agc cgg gag gtt cag cag tcc tgg ccc			393
Tyr Ile His Arg Ile Pro Xaa Ser Arg Glu Val Gln Gln Ser Trp Pro			
90	95	100	
tcc acc gtt tyc acc acc ttg cac tcc atg tgg ctc tcc ttk ccc cta			441
Ser Thr Val Xaa Thr Thr Leu His Ser Met Trp Leu Ser Xaa Pro Leu			
105	110	115	
att cac agg gtg aag cca rat ttg gtg ttg tgt aac gga cca gga aca			489
Ile His Arg Val Lys Pro Xaa Leu Val Leu Cys Asn Gly Pro Gly Thr			
120	125	130	
tgt gty cct atc tgt gta tct gcc ctt ctc ctt ggg ata cta gga ata			537
Cys Val Pro Ile Cys Val Ser Ala Leu Leu Leu Gly Ile Leu Gly Ile			
135	140	145	
aag aaa gtg atc att gtc tac gtt gaa agc atc tgc cgt gta aaa acs			585
Lys Lys Val Ile Ile Val Tyr Val Glu Ser Ile Cys Arg Val Lys Thr			
150	155	160	165
tta tcc atg tcc gga aag att ctg ttt cat ctc tca aat tac ttc att			633
Leu Ser Met Ser Gly Lys Ile Leu Phe His Leu Ser Asn Tyr Phe Ile			
170	175	180	
gtt cag tgg ccg gct ctg aaa gaa aag tat ccc aaa tcg gtg tac ctt			681
Val Gln Trp Pro Ala Leu Lys Glu Lys Tyr Pro Lys Ser Val Tyr Leu			
185	190	195	
ggg cga att gtt tgacaaatgg caactgactt ctttagaatt ttgcasttaa			733
Gly Arg Ile Val			
200			
cagtartatg tactcaaatt ggggggaaaa aaaccctaca tgttttcttgt aaaggcgtct			793
gacagtcctg araattattg atggtaagga ataaaaaatg twcagatrac tcagtgaara			853
aactgaggct tctcttatga aacaaacatt gataaacgta actacyaaat gtttatgcct			913
ctgtaaacca aattttctttt ctarataaaaa atatgtatta ctacctgcaa aaaaaaaaaa			973

<210> 357

<211> 868

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 126..527

<221> sig_peptide

<222> 126..182

<223> Von Heijne matrix

score 3.90000009536743

seq ILFHGVFYAGGFA/IV

<221> polyA_signal

<222> 834..839

<221> polyA_site

<222> 856..867

<400> 357

actggaagaa ctgcgtcatgc tctttgtagc gtgggtgcttc tgttgctcac aggacaactt 60

gcctttgatg attttcaaga gagttgtgct atgatgtggc aaagtatgca ggaagcaggc 120

gggtca atg cct ctg gga gca agg atc ctt ttc cac ggt gtg ttc tat gcc 170

Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala

```

ggg ggc ttt gcc att gtg tat tac ctc att caa aag ttt cat tcc agg      218
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
      1              5              10
act tta tat tac aag ttg gca gtg gar cag ctg car arc cat ccc gag      266
Thr Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Xaa His Pro Glu
      15              20              25
gca cag gaa gct ctg ggc cct cct ctc aac atc cat tat ctc aag ctc      314
Ala Gln Glu Ala Leu Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu
      30              35              40
atc gac agg gaa aac ttc gtg gac att gtt rat gcc aag ttg aaa att      362
Ile Asp Arg Glu Asn Phe Val Asp Ile Val Xaa Ala Lys Leu Lys Ile
      45              50              55              60
cct gtc tct gga tcc aaa tca gag ggc ctt ctc tac gtc cac tca tcc      410
Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser
      65              70              75
aga ggt ggc ccc ttt cag agg tgg cac ctt gac gag gtc ttt tta gag      458
Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu
      80              85              90
ctc aag gat ggt cag cag att cct gtg ttc aag ctc agt ggg gaa aac      506
Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn
      95              100              105
ggg gat gaa gtg aaa aag gag tagagacgac ccagaagacc cagcttgctt      557
Gly Asp Glu Val Lys Lys Glu
      110              115
ctagtccatc cttccctcat ctctaccata tggccactgg ggtgggtggcc catctcagtg      617
acagacactc ctgcaaccca gktttccagc caccagtggg atgatgggtat gtgccagcac      677
atggtaattt tgggtgaatt ctaacttggg cacaacgaat gctatttgct atttttaaac      737
tgaatccgaa agaaactcct attataaatt taagataatg taatgtattt gaaagtgctt      797
tgtataaaaa agcacatgat aaaaggaatc agaattaata aaatgtttgt tgatctttaa      857
aaaaaaaaaa h                                                                868

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<210> 358
 <211> 519
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 66..320

<221> sig_peptide
 <222> 66..113
 <223> Von Heijne matrix
 score 3.5
 seq TALAAXTWLGVWG/VR

<221> polyA_signal
 <222> 490..495

<221> polyA_site
 <222> 508..519

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<400> 358
aattagcgcg taacgcasag actgcttgct gcggcagaga cgccagakgt gcagctccag      60
cagca atg gca gtg acg gcg ttg gcg gcg mrg acg tgg ctt ggc gtg tgg      110
      Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp
      -15              -10              -5
ggc gtg agg acc atg caa gcc cga ggc ttc gcc tcg gat cag tcc gag      158
Gly Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu
      1              5              10              15

```

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aat gtc gac cgg ggc gcg ggc tcc atc cgg gaa gcc ggt ggg gcc ttc      206
Asn Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe
                20                25                30
gga aag aga gag cag gct gaa gag gaa cga tat ttc cga gca cag agt      254
Gly Lys Arg Glu Gln Ala Glu Glu Glu Arg Tyr Phe Arg Ala Gln Ser
                35                40                45
aca gaa caa ctg gca rct ttg aaa aaa crc cat gaa gaa gar atc gtt      302
Thr Glu Gln Leu Ala Xaa Leu Lys Lys Xaa His Glu Glu Glu Ile Val
                50                55                60
cat cat aga gaa gga gat tgagcgtctg cagaaagaaa ttgagcgcca      350
His His Arg Glu Gly Asp
        65
taagcagaag atcaaaatgc tagaacatga tgattaagtg cacaccgtgt gccatagaat      410
ggcacatgtc attgccact tctgtgtaaa catggttctg gtttaactaa tatttgtctg      470
tgtgtacta acagattata ataaattgtc atcagtga aa aaaaaaaa      519

```

<210> 359
 <211> 1028
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 73..948

<221> sig_peptide
 <222> 73..159
 <223> Von Heijne matrix
 score 4.40000009536743
 seq IVLHLVLQGMVYT/EY

<221> polyA_site
 <222> 1016..1028

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<400> 359
agctttaag gcctggccag gggaggagca cagatatttt cctgtataat tccagaatgt      60
cttcagagag cc atg cat gga ttg ctt cat tac ctt ttc cat acg aga aac      111
                Met His Gly Leu Leu His Tyr Leu Phe His Thr Arg Asn
                -25                -20
cac acc ttc att gtc ctg cac ctg gtc ttg caa ggg atg gtt tat act      159
His Thr Phe Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr Thr
        -15                -10                -5
gag tac acc tgg gaa gta ttt ggc tac tgt cag gag ctg gag ttg tcc      207
Glu Tyr Thr Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu Ser
        1                5                10                15
ttg cat tac ctt ctt ctg ccc tat ctg ctg cta ggt gta aac ctg ttt      255
Leu His Tyr Leu Leu Leu Pro Tyr Leu Leu Gly Val Asn Leu Phe
                20                25                30
ttt ttc acc ctg act tgt gga acc aat cct ggc att ata aca aaa gca      303
Phe Phe Thr Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys Ala
                35                40                45
aat gaa tta tta ttt ctt cat gtt tat gaa ttt gat gaa ktg atg ttt      351
Asn Glu Leu Leu Phe Leu His Val Tyr Glu Phe Asp Glu Xaa Met Phe
        50                55                60
cca aaa aac gtg agg tgc tct act tgt gat tta agg aaa cca gct cga      399
Pro Lys Asn Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala Arg
        65                70                75                80
tcc aas cac tgc akt gtg tgt aac tgg tgt cac cgt ttc rac cat      447
Ser Xaa His Cys Xaa Val Cys Asn Trp Cys Val His Arg Phe Xaa His
                85                90                95

```

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cac tgt gtt tgg gtg aac aac tgc atc ggg gcc tgg aac atc agg tmc      495
His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg Xaa
      100                      105                      110
ttc ctc atc tac gtc ttg acc ttg acg gcc tcg gct gcc acc gtc gcc      543
Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val Ala
      115                      120                      125
att gtg agc acc act ttt ctg gtc cac ttg gtg gtg atg tca gat tta      591
Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp Leu
      130                      135                      140
tac cag gag act tac atc gat gac ctt gga cac ctc cat gtt atg gac      639
Tyr Gln Glu Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met Asp
      145                      150                      155                      160
acg gtc ttt ctt att cag tac ctg ttc ctg act ttt cca cgg att gtc      687
Thr Val Phe Leu Ile Gln Tyr Leu Phe Leu Thr Phe Pro Arg Ile Val
      165                      170                      175
ttc atg ctg ggc ttt gtc gtg gtt ctg arc ttc ctc ctg ggt ggc tac      735
Phe Met Leu Gly Phe Val Val Val Leu Xaa Phe Leu Leu Gly Gly Tyr
      180                      185                      190
ctg ttg ttt gtc ctg tat ctg gcg gcc acc aac cag act act aac gag      783
Leu Leu Phe Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn Glu
      195                      200                      205
tgg tac aga rgt gac tgg gcc tgg tgc cag cgt tgt ccc ctt gtg gcc      831
Trp Tyr Arg Xaa Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val Ala
      210                      215                      220
tgg cct ccg tca gca gar ccc caa gtc cac cgg aac att cac tcc cat      879
Trp Pro Pro Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser His
      225                      230                      235                      240
ggg ctt cgg arc aac ctt caa gar atc ttt cta cct gcc ttt cca tgt      927
Gly Leu Arg Xaa Asn Leu Gln Glu Ile Phe Leu Pro Ala Phe Pro Cys
      245                      250                      255
cat gag agg aag aaa caa gaa tgacmagtgt atgactgcct ttgagctgta      978
His Glu Arg Lys Lys Gln Glu
      260
gttcccgttt atttacacat gtggatcctc gttttccaaa aaaaaaaaaa      1028

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<210> 360

<211> 452

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 69..434

<221> sig_peptide

<222> 69..236

<223> Von Heijne matrix

score 4.90000009536743

seq FACVPGASPTTLA/FP

<221> polyA_signal

<222> 419..424

<221> polyA_site

<222> 441..452

<400> 360

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acagcgtgas tcgcccgccga gaagaatatg aaaaagcaga gcganctcgg ttaaggga    60
gcgccgag atg acg ggc ttt ctg ctg ccg ccc gca agc aga ggg act cgg    110
      Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg

```

```

          -55          -50          -45
aga tca tgc agc aga agc aga aaa agg caa acg aga aga agg agg aac      158
Arg Ser Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn
          -40          -35          -30
cca agt agc ttt gtg gct tcg tgt cca acc ctc ttg ccc ttc gcc tgt      206
Pro Ser Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys
          -25          -20          -15
gtg cct gga gcc agt ccc acc acg ctc gcg ttt cct cct gta ktg ctc      254
Val Pro Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Xaa Leu
          -10          -5          1          5
aca ggt ccc avc acc gat ggc att ccc ttt gcc ctr nak tct gca gcg      302
Thr Gly Pro Xaa Thr Asp Gly Ile Pro Phe Ala Leu Xaa Ser Ala Ala
          10          15          20
ggt ccc ttt tgt gct tcc ttc ccc tca ggt avc ctc tct ccc cct ggg      350
Gly Pro Phe Cys Ala Ser Phe Pro Ser Gly Xaa Leu Ser Pro Pro Gly
          25          30          35
cca ctc ccg ggg gtg agg ggg tta ccc ctt ccc agt gtt ttt tat tcc      398
Pro Leu Pro Gly Val Arg Gly Leu Pro Leu Pro Ser Val Phe Tyr Ser
          40          45          50
tgt ggg gct cac ccc aaa gta tta aaa gta gct ttg taattcaaaa      444
Cys Gly Ala His Pro Lys Val Leu Lys Val Ala Leu
55          60          65
aaaaaaaaa      452

```

<210> 361

<211> 875

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 628..804

<221> sig_peptide

<222> 628..711

<223> Von Heijne matrix

score 4.19999980926514

seq LMPVIPALQEAXA/GG

<221> polyA_site

<222> 864..875

<400> 361

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aaagatggac accgcggagg aagacatatg tagagtgtgt cggtcagaag gaacacctga      60
gaaaccgctt tatcatcctt gtgtatgtac tggcagtatt aagttngtcc atcaagaatg      120
cttagttcaa tggctgaaac acagtcgaaa agaatactgt gaattatgca agcacagatt      180
tgcttttaca ccaattttatt ctccagatat gccttcacgg cttccaattc aagacatatt      240
tgctggactg gttacaagta ttggcactgc aatacगतat tggtttcatt atacacttgt      300
ggcctttgca ttggtggggag ttgttcctct tacagcatgt gagtattcat gcctctgatt      360
ggagttattt aaacattgca taactactta atattataaa gcaatattgc atcatattat      420
tatttgactg atgtttagtt atttgatgtc agagtgtcat gtattaggaa agccttactt      480
araaratggt catcggaact aaraatgakt ttaacaggtc agttttttga gtgaatgtgg      540
gaaaraacac agcatacaga atggctaacc atgaaagtgc atgaaagcgt kgaaaaaatc      600
aatcaaatc ataattagat atgaagt atg cta rag ctt tca agg gct aca aaa      654
Met Leu Xaa Leu Ser Arg Ala Thr Lys
          -25          -20
rac ggc cgg gcg cgg tgg ctt atg cct gta atc cca gca ctt cag gag      702
Xaa Gly Arg Ala Arg Trp Leu Met Pro Val Ile Pro Ala Leu Gln Glu
          -15          -10          -5
gcc gan gca ggc gga tca cga ggt cag gag ttt gaa act agc ctg gcc      750

```

Ala Xaa Ala Gly Gly Ser Arg Gly Gln Glu Phe Glu Thr Ser Leu Ala
 1 5 10
 aac atg gag act gag gca gga gaa ttg ctt aaa ccc agg agg cgg agg 798
 Asn Met Glu Thr Glu Ala Gly Glu Leu Leu Lys Pro Arg Arg Arg Arg
 15 20 25
 ttg car tgaactgaga tcgcaccact gcactccagc ttgggcaaca gagcaagact 854
 Leu Gln
 30
 ttgtctcgca aaaaaaaaaa a 875

<210> 362
 <211> 531
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..366

<221> sig_peptide
 <222> 70..108
 <223> Von Heijne matrix
 score 3.5
 seq MHLLSNWANPASS/RR

<221> polyA_signal
 <222> 496..501

<221> polyA_site
 <222> 521..531

<400> 362
 aagtggccat ggcggatata ggcactacag catcggcggc ggcggctagt gccgctagcg 60
 cctcgagcg atg cac ctc ctt tcc aac tgg gca aac ccc gct tcc agc aga 111
 Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg
 -10 -5 1
 cgt cct tct atg gcc gct tca ggc act tct tgg ata tca tcg acc ctc 159
 Arg Pro Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu
 5 10 15
 gca cac tct ttg tca ctg aga gac gtc tca gag agg ctg tgc agc tgc 207
 Ala His Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys
 20 25 30
 tgg agg act ata agc atg gga ccc tgc gcc cgg ggg tca cca atg aac 255
 Trp Arg Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn
 35 40 45
 agc tct gga gtg cac aga aaa tca agc agg cta ttc tac atc cgg aca 303
 Ser Ser Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr
 50 55 60 65
 cca atg aga aga tct tca tgc cat tta gaa tgt crg gtt ata ttc ctt 351
 Pro Met Arg Arg Ser Ser Cys His Leu Glu Cys Xaa Val Ile Phe Leu
 70 75 80
 ttg gga cgc caa ttg taaktgttac cttcaaagga tttccttttc taaaaaatta 406
 Leu Gly Arg Gln Leu
 85
 ttttaratgt ctaactttat gttattgtc acgggtatatt gactgaattg ttgatttagg 466
 ataagtcaat tcttggaggg aaattaccaa ataaaatgat atgtattttc taccacaaaa 526
 aaaaa 531

<210> 363
 <211> 1244
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..366

<221> sig_peptide
 <222> 70..108
 <223> Von Heijne matrix
 score 3.5
 seq MHLLSNWANPASS/RR

<221> polyA_site
 <222> 1233..1244

<400> 363
 aagtggccat ggcggataca gcgactacag catcggcggc ggcggctagt gccgctagcg 60
 cctcgagcgc atg cac ctc ctt tcc aac tgg gca aac ccc gct tcc agc aga 111
 - Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg
 -10 -5 1
 cgt cct tct atg gcc gct tca ggc act tct tgg ata tca tcg acc ctc 159
 Arg Pro Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu
 5 10 15
 gca cac tct ttg tca ctg aga gac gtc tca gag agg ctg tgc agc tgc 207
 Ala His Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys
 20 25 30
 tgg agg act ata agc atg gga ccc tgc gcc cgg ggg tca cca atg aac 255
 Trp Arg Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn
 35 40 45
 agc tct gga gtg cac aga aaa tca agc agg cta ttc tac atc cgg aca 303
 Ser Ser Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr
 50 55 60 65
 cca atg aga aga tct tca tgc cat tta raa tgt cag gtt ata ttc ctt 351
 Pro Met Arg Arg Ser Ser Cys His Leu Xaa Cys Gln Val Ile Phe Leu
 70 75 80
 ttg gga cgc caa ttg tagtcggtct tctcttgccc aaccagacac tggcatccac 406
 Leu Gly Arg Gln Leu
 85
 tgtcttcttg cagtggctga accagagcca caatgcctgt gtcaactatg caaaccgcaa 466
 tgraccaag ccttcacctg catccaagtt catccaggga tacctgggag ctgtcatcag 526
 cgccgtctcc attgctgttg gccttatktc ctggttcaga aagccaacaa gttcacccca 586
 gccaccgcc ttctcatcca gaggtttgtg ccgttccttg ctgtagccag tgccaatata 646
 tgcaatgttg tctgatgag gtacggggag ctggaggaag ggattgatgt cctggacagc 706
 gatggcaacc tcgtgggctc ctccaagatc gcagcccgac acgccctgct ggagacggcg 766
 ctgacgcgag tggctctgcc catgcccata ctggtgttac ccccgatcgt catgtccatg 826
 ctggagaaga cggctctcct gcaggcacgc ccccggtgct tcttccctgt gcaaagcctc 886
 gtgtgccttg cagccttcgg cctggccctg ccgctggcca tcagcctctt cccgcaaata 946
 tcagagattg aaacatccca attagagccg gagatagccc aggccacgag cagccggaca 1006
 gtggtgtaca acaaggggtt gtgagtgttg tcagggcctt ggggacggag cactgtgcag 1066
 ccggggagct gaggggcarg gccgtagact cacggctgca cctgcaggga gcagcacgcc 1126
 aacccagca gtcctgggcc ccctgggaga gtgctcaacc tacagtggag ggagactgac 1186
 ccattcacat tttaacatag gcaagaggag ttctaacaca tttcgtacaa aaaaaaaaa 1244

<210> 364
 <211> 631
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 111..434

<221> sig_peptide

<222> 111..185

<223> Von Heijne matrix
 score 3.90000009536743
 seq WIAAVTIAAGTAA/IG

<221> polyA_site

<222> 618..631

<400> 364

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aatcgcgagg tcggtgcttt agtacgccgc tggcaccttt actctcgccg gccgcgcgaa      60
cccgtttgag ctcggtatcc tagtgacac gccttgcaag cgacggcgcc atg agt      116
                                     Met Ser
                                     -25
ctg act tcc agt tcc agc gta cga gtt gaa tgg atc gca gca gtt acc      164
Leu Thr Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala Val Thr
          -20          -15          -10
att gct gct ggg aca gct gca att ggt tat cta gct tac aaa aga ttt      212
Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys Arg Phe
          -5          1          5
tat gtt aaa gat cat cga aat aaa gct atg ata aac ctt cac atc cag      260
Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His Ile Gln
10          15          20          25
aaa gac aac ccc aag ata gta cat gct ttt gac atg gag gat ttg gga      308
Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp Leu Gly
          30          35          40
gat aaa gct gtg tac tgc cgt tgt tgg agg tcc aaa aag ttc cca ttc      356
Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe Pro Phe
          45          50          55
tgt gat ggg gct cac aca aaa cat aac gaa gag act gga gac aat gtg      404
Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp Asn Val
          60          65          70
ggc cct ctg atc atc aag aaa aaa gaa act taaatggaca cttttgatgc      454
Gly Pro Leu Ile Ile Lys Lys Lys Glu Thr
          75          80
tgcaaatcag cttgtcgtga agttacctga ttgtttaatt araatgacta ccacctctgt      514
ctgattcacc ttcgctggat tctaaatgtg gtatattgcm aactgcagct ttcacattta      574
tggcatttgt cttgttgaaa catcgtggtg cacatttgtt taaacaaaaa aaaaaaa      631

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<210> 365

<211> 781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 19..567

<221> sig_peptide

<222> 19..63

<223> Von Heijne matrix
 score 8.39999961853027
 seq AMWLLCVALAVLA/WG

<221> polyA_signal

<222> 749..754

<221> polyA_site

<222> 771..781

<400> 365

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aagtgtgtgt taccatc atg gaa gca atg tgg ctc ctg tgt gtg gcg ttg      51
                        Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu
                        -15                -10                -5
gcg gtc ttg gca tgg ggc ttc ctc tgg gtt tgg gac tcc tca gaa cga      99
Ala Val Leu Ala Trp Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg
                        1                5                10
atg aag agt cgg gag cag gga aga cgg ctg gga gcc gaa agc cgg acc     147
Met Lys Ser Arg Glu Gln Gly Arg Arg Leu Gly Ala Glu Ser Arg Thr
                        15                20                25
ctg ctg gtc ata gcg cac cct gac gat gaa gcc atg ttt ttt gct ccc     195
Leu Leu Val Ile Ala His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro
                        30                35                40
aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc     243
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys
45                50                55                60
ttc tct gca gga aat tac tac aat caa gga gag act cgt aag aaa gaa     291
Phe Ser Ala Gly Asn Tyr Tyr Asn Gln Gly Glu Thr Arg Lys Lys Glu
                        65                70                75
ctt ttg car agc tgt gat gtt ttg ggg att cca ctc tcc agt gta atg     339
Leu Leu Gln Ser Cys Asp Val Leu Gly Ile Pro Leu Ser Ser Val Met
                        80                85                90
att att gac aac agg gat ttc cca rat gac cca ggc atg cag tgg gac     387
Ile Ile Asp Asn Arg Asp Phe Pro Xaa Asp Pro Gly Met Gln Trp Asp
                        95                100               105
aca rag cac gtg gcc ara gtc ctc ctt cag cac ata gaa gtg aat ggc     435
Thr Xaa His Val Ala Xaa Val Leu Leu Gln His Ile Glu Val Asn Gly
110               115               120
atc aat ctg gtg gtg act ttc gat gca ggg gga rta agt ggc cac agc     483
Ile Asn Leu Val Val Thr Phe Asp Ala Gly Gly Xaa Ser Gly His Ser
125               130               135               140
aat cac att gct ctg tat gca gct gtg agg aag ctt gag ggc caa att     531
Asn His Ile Ala Leu Tyr Ala Ala Val Arg Lys Leu Glu Gly Gln Ile
                        145                150                155
tgc aag ccc tgt ggc act gga caa gac ttt aag gaa tgagtgtgt          577
Cys Lys Pro Cys Gly Thr Gly Gln Asp Phe Lys Glu
                        160                165
caatcagtgt gcctccacct tcaccatctt cttcccctta ctctcacttc cgtcagtgtg 637
ttatatacaac tctcaaatct ttcttgagga aggaggatat acatacataa tatgaaatgt 697
gtttgttctt cacagtcacc cgattttact gatatttatt tgcattttac caataaaaag 757
aaaatgcaag ctcaaaaaaa aaaa                                         781

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<210> 366

<211> 931

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 19..312

<221> sig_peptide

<222> 19..63

<223> Von Heijne matrix
score 8.39999961853027

seq AMWLLCVALAVLA/WG

<221> polyA_signal

<222> 896..901

<221> polyA_site

<222> 921..931

<400> 366

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aagtgtgtgct tacccatc atg gaa gca atg tgg ctc ctg tgt gtg gcg ttg      51
                        Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu
                        -15                -10                -5
gcg gtc ttg gca tgg ggc ttc ctc tgg gtt tgg gac tcc tca gaa cga      99
Ala Val Leu Ala Trp Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg
                        1                5                10
atg aag agt cgg gag cag gga rga cgg ctg gga gcc gaa agc cgg acc     147
Met Lys Ser Arg Glu Gln Gly Xaa Arg Leu Gly Ala Glu Ser Arg Thr
                        15                20                25
ctg ctg gtc ata gcg cac cct gac gat gaa gcc atg ttt ttt gct ccc     195
Leu Leu Val Ile Ala His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro
                        30                35                40
aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc     243
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys
45                50                55                60
ttc tct gca gtt ttc cgt agg gag cta agt gaa tac acc gaa rgt ctt     291
Phe Ser Ala Val Phe Arg Arg Glu Leu Ser Glu Tyr Thr Glu Xaa Leu
                        65                70                75
acc tct gaa ccc ctc ama gcc tagggacagg arcggccggc ttacctggtg     342
Thr Ser Glu Pro Leu Xaa Ala
                        80
ggttggggga cgtcggcagc tcrctacta cgccagcagg attganganc acagaaacag     402
ttgchsttgg ttgtattcag tacctkcatt tccgttggga actccaccwg tacttggtat     462
kctgtggaac ttttttttat ttgtagaagg agcaagaata ttgaccttac tatatagcac     522
acgaaacaat ctatgctgta tcgtgcctgc tcaatcctta aagttaactt ctaatgatag     582
taaaaracct tcctgctgcc tttaaaatgc agcttgtgct aktaacatgc atgtgtcaaa     642
ttgaaraatt agacatagat gactaratar aaagtaattt tgtaggtaat ttaragttc     702
aactccaccc agctttcakt gaaggaacct ttcaaataat aratttttgc ttaccatara     762
raaaaratca aatgacaaag caaatattga ccattaagct ggaatatggt gataattgaa     822
cagttgtata aatgaaktaa ttgaattgta cacatacaat ggggtgaattt tatggcatgt     882
caaagtatac ctcaataaag ctattttttt aaattgcmay aaaaaaaaaa     931

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<210> 367

<211> 849

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 64..612

<221> sig_peptide

<222> 64..234

<223> Von Heijne matrix

score 3.79999995231628

seq QLWLVMFCGAGS/VT

<221> polyA_site

<222> 839..849

<400> 367

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acatacgggc aagtttataa gggtcgtcat gtcaaaacgg gccagcttgc agccatcaag      60
gtt atg gat gtc aca ggg gat gaa gag gaa gaa atc aaa caa gaa att      108
  Met Asp Val Thr Gly Asp Glu Glu Glu Ile Lys Gln Glu Ile
      -55      -50      -45
aac atg ttg aag aaa tat tct cat cac cgg aat att gct aca tac tat      156
Asn Met Leu Lys Lys Tyr Ser His His Arg Asn Ile Ala Thr Tyr Tyr
      -40      -35      -30
ggg gct ttt atc aaa aag aac cca cca ggc atg gat gac caa ctt tgg      204
Gly Ala Phe Ile Lys Lys Asn Pro Pro Gly Met Asp Asp Gln Leu Trp
      -25      -20      -15
ttg gtg atg gag ttt tgt ggt gct ggc tct gtc acc gac ctg atc aag      252
Leu Val Met Glu Phe Cys Gly Ala Gly Ser Val Thr Asp Leu Ile Lys
      -10      -5      1      5
aac aca aaa ggt aac acg ttg aaa gag gag tgg att gca tac atc tgc      300
Asn Thr Lys Gly Asn Thr Leu Lys Glu Glu Trp Ile Ala Tyr Ile Cys
      10      15      20
msg gaa atc tta cgg ggg ctg art cac ctg cac cag cat aaa gtg att      348
Xaa Glu Ile Leu Arg Gly Leu Xaa His Leu His Gln His Lys Val Ile
      25      30      35
cat cga rat att aaa ggg caa aat gtc ttg ctg act gaa aat gca gaa      396
His Arg Xaa Ile Lys Gly Gln Asn Val Leu Leu Thr Glu Asn Ala Glu
      40      45      50
gtt aaa cta gtg gac ttt gga rtc akt gct cag ctt gat cga aca gtg      444
Val Lys Leu Val Asp Phe Gly Xaa Xaa Ala Gln Leu Asp Arg Thr Val
      55      60      65      70
ggc agg arg aat act ttc att gga act ccc tac tgg atg gca cca raa      492
Gly Arg Xaa Asn Thr Phe Ile Gly Thr Pro Tyr Trp Met Ala Pro Xaa
      75      80      85
gtt att gcc tgt gat gaa aac cca sat gcc aca tat gat ttc aar art      540
Val Ile Ala Cys Asp Glu Asn Pro Xaa Ala Thr Tyr Asp Phe Lys Xaa
      90      95      100
gac ttg tgg tct ttg ggt atc acc gcc att gaa atg gca gaa ggg ctc      588
Asp Leu Trp Ser Leu Gly Ile Thr Ala Ile Glu Met Ala Glu Gly Leu
      105      110      115
ccc ctc tct gtg aca tgc acc cca tgagagctct cttcctcatc ccccggaatc      642
Pro Leu Ser Val Thr Cys Thr Pro
      120      125
cagcgccctcg gctgaagtct aagaagtggg caaaaaaatt ccagtcattt attgagagct      702
gcttggtaaa aaatcacagc cagcgaccag caacagaaca attgatgaag catccattta      762
tacgagacca acctaataag cgacaggtcc gcattcaact caaggaccat attgatagaa      822
caaagaagaa gcgaggaaaa aaaaaaa      849

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<210> 368

<211> 644

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 39..458

<221> sig_peptide

<222> 39..80

<223> Von Heijne matrix

score 4.40000009536743

seq FLTALLWRGRIPG/RQ

<221> polyA_signal

<222> 613..618

<221> polyA_site

<222> 633..644

<400> 368

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agcggagacg cagagtcttg agcagcgcn caggcacc atg ttc ctg act gcg ctc      56
                                   Met Phe Leu Thr Ala Leu
                                   -10
ctc tgg cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg      104
Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg
      -5                               1                               5
cgg ccg cgg ttc gtg tgc ttg cgc gcc aag cag aac atg atc cgc cgc      152
Arg Pro Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg
      10                               15                               20
ctg gag atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg      200
Leu Glu Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met
      25                               30                               35                               40
acc cgg gag cag gag cgc ggc cac gcc gcg ttg cgc agg agg gag gcc      248
Thr Arg Glu Gln Glu Arg Gly His Ala Ala Leu Arg Arg Arg Glu Ala
      45                               50                               55
ttc gag gcc ata aag gcg gcc gcc act tcc aag ttc ccc ccg cat aga      296
Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg
      60                               65                               70
ttc att gcg gac cag ctc gac cat ctc aat vgt cac caa gaa atg gtc      344
Phe Ile Ala Asp Gln Leu Asp His Leu Asn Xaa His Gln Glu Met Val
      75                               80                               85
cta atc ctg agt cgt cac cct tgg att tta tgg atc acg gag ctg acc      392
Leu Ile Leu Ser Arg His Pro Trp Ile Leu Trp Ile Thr Glu Leu Thr
      90                               95                               100
atc ttt acc tgg tct gga ctg aaa aac tgt agc ttg tgt gaa aat gag      440
Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys Ser Leu Cys Glu Asn Glu
      105                               110                               115                               120
ctt tgg acc agt ctt tat taaaacaaac aaacatgagt agtctgcata      488
Leu Trp Thr Ser Leu Tyr
      125
tcgaatatct agagctctaa acccccctaat acttaaaagt ctaattgctg tcctgtgggt      548
tcattagtct gataggaaga tagggatttc ctgagtcaca gatgatattt tgaaggaaag      608
ctgcaataaa gccacaatga tttgaaaaaa aaaaaa      644

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<210> 369

<211> 918

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 9..185

<221> sig_peptide

<222> 9..50

<223> Von Heijne matrix

score 3.70000004768372

seq AALVTVLFTGVRR/LH

<221> polyA_site

<222> 906..918

<400> 369

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agctcagc atg gct gct tta gtg act gtt ctc ttc aca ggt gtc cgg agg      50
      Met Ala Ala Leu Val Thr Val Leu Phe Thr Gly Val Arg Arg

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-10

-5

```

ctg cac tgc agc gcr scg ctt ggg cgg gcg gcc agt ggc grc tac agc      98
Leu His Cys Ser Ala Xaa Leu Gly Arg Ala Ala Ser Gly Xaa Tyr Ser
1          5          10          15
agg aac tgg ctg cca acc cct ccg gct acg ggc ccc tta ccg agc tcc      146
Arg Asn Trp Leu Pro Thr Pro Pro Ala Thr Gly Pro Leu Pro Ser Ser
          20          25          30
cag act ggt cat atg cgg atg gcc gcc ctg ctc ccc caa tgaaaggcca      195
Gln Thr Gly His Met Arg Met Ala Ala Leu Leu Pro Gln
          35          40          45
gcttcgaaaa aaagctgaaa gggagacktt tgcaaracra kttgtactgc tgtcacagga      255
aatggacgct ggattacaas catggcasct caggcagcar aakttgcagg aaraacaaag      315
gaagcaggaa aatgctctta aacccaaagg ggcttcactg aaaascccac ttccaaktca      375
ataaaaaagca actcctgcct cccttcctca ccctgtctct ggatttcttt tctatcacct      435
aratgcttca tccagccara aaatagcctt cackktcccc atctgtcttc aragcaaaar      495
agctgggacm ccaaraacaa gctgttarat cactgcctgg gaggcttggc ttartactct      555
catctctggt tccattccag ttcagctaag tcttgcttta aaatttttac ctccatagctg      615
ggtgcggtgg ctacgcctg taatcccagc actttgggag gctgaggcgg gcagatcaca      675
agatcaggag ttcgagacca gcctggccaa cccagcctgg tcaacatggt gaaaccctgt      735
ccctactaaa gatacaacaa attagccggg cgtggtgggg tgcgcttgta atcccagcta      795
ctcaggaggc tgaggcagga gaatcgctta aactcgggag gtagagggtg cagtgaacca      855
aggtcacacc attgcactcc aacctgggag acagggcgag actctgtctc aaaaaaaaaa      915
aaa                                                                918

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<210> 370

<211> 472

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 14..316

<221> sig_peptide

<222> 14..121

<223> Von Heijne matrix

score 5.19999980926514

seq PLRLNLLILIEG/SV

<221> polyA_signal

<222> 442..447

<221> polyA_site

<222> 458..471

<400> 370

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attatataga gcc atg ggg cct tac aac gtg gca gtg cct tca gat gta      49
          Met Gly Pro Tyr Asn Val Ala Val Pro Ser Asp Val
          -35          -30          -25
tct cat gcc cgc ttt tat ttc tta ttt cat cga cca tta agg ctg tta      97
Ser His Ala Arg Phe Tyr Phe Leu Phe His Arg Pro Leu Arg Leu Leu
          -20          -15          -10
aat ctg ctc atc ctt att gag ggc agt gtc gtc ttc tat cag ctc tat      145
Asn Leu Leu Ile Leu Ile Glu Gly Ser Val Val Phe Tyr Gln Leu Tyr
          -5          1          5
tcc ttg ctg cgg tcg gag aag tgg aac cac aca ctt tcc atg gct ctc      193
Ser Leu Leu Arg Ser Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu
          10          15          20
atc ctc ttc tgc aac tac tat gtt tta ttt aaa ctt ctc cgg gac aga      241
Ile Leu Phe Cys Asn Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg
          25          30          35          40

```

```

wta kta tta ggc agg gca tac tcc tac cca ctc aac agt tat gaa ctc      289
Xaa Xaa Leu Gly Arg Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu
      45                      50                      55
aag gca aac twa gct gcc tct caw caa tgagggagaa ctcagataaa      336
Lys Ala Asn Xaa Ala Ala Ser Xaa Gln
      60                      65
aatattttca tacgttctat ttttttcttg tgatttttat aaatatttaa gatattttat      396
attttgtata ctattatggt ttgaaagtcg ggaagagtaa gggatattaa atgtatccgt      456
aaacaaaaaa aaaaam      472

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<210> 371

<211> 1504

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 70..1092

<221> sig_peptide

<222> 70..234

<223> Von Heijne matrix

score 4.09999990463257

seq AVCAALLASHPTA/EV

<221> polyA_signal

<222> 1475..1480

<221> polyA_site

<222> 1493..1504

<400> 371

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agaaatcgta ggacttccga aagcagcggc ggcgtttgct tcactgcttg gaagtgtgag      60
tgcgcggaag atg cga aag gtg gtt ttr att acc ggg gct agc agt ggc att      111
      Met Arg Lys Val Val Leu Ile Thr Gly Ala Ser Ser Gly Ile
      -55                      -50                      -45
ggc ctg gcc ctc tgc aag cgg ctg ctg gcg gaa gat gat gag ctt cat      159
Gly Leu Ala Leu Cys Lys Arg Leu Leu Ala Glu Asp Asp Glu Leu His
      -40                      -35                      -30
ctg tgt ttg gcg tgc agg aat atg agc aag gca gaa gct gtc tgt gct      207
Leu Cys Leu Ala Cys Arg Asn Met Ser Lys Ala Glu Ala Val Cys Ala
      -25                      -20                      -15                      -10
gct ctg ctg gcc tct cac ccc act gct gag gtc acc att gtc cag gtg      255
Ala Leu Leu Ala Ser His Pro Thr Ala Glu Val Thr Ile Val Gln Val
      -5                      1                      5
gat gtc agc aac ctg cag tca ttc ttc cgg gcc tcc aag gaa ctt aag      303
Asp Val Ser Asn Leu Gln Ser Phe Phe Arg Ala Ser Lys Glu Leu Lys
      10                      15                      20
caa agg ttt cag aga tta gac tgt ata tat cta aat gct ggg atc atg      351
Gln Arg Phe Gln Arg Leu Asp Cys Ile Tyr Leu Asn Ala Gly Ile Met
      25                      30                      35
cct aat cca caa cta aat atc aaa gca ctt ttc ttt ggc ctc ttt tca      399
Pro Asn Pro Gln Leu Asn Ile Lys Ala Leu Phe Phe Gly Leu Phe Ser
      40                      45                      50                      55
aga aaa gtg att cat atg ttc tcc aca gct gaa ggc ctg ctg acc cag      447
Arg Lys Val Ile His Met Phe Ser Thr Ala Glu Gly Leu Leu Thr Gln
      60                      65                      70
ggg gat aag atc act gct gat gga ctt cag gag gtg ttt gag acc aat      495
Gly Asp Lys Ile Thr Ala Asp Gly Leu Gln Glu Val Phe Glu Thr Asn
      75                      80                      85

```



```

gtc ttt ggc cat ttt atc ctg att cgg gaa ctg gag cct ctc ctc tgt      543
Val Phe Gly His Phe Ile Leu Ile Arg Glu Leu Glu Pro Leu Leu Cys
      90                      95                      100
cac agt gac aat cca tct cag ctc atc tgg aca tca tct cgc agt gca      591
His Ser Asp Asn Pro Ser Gln Leu Ile Trp Thr Ser Ser Arg Ser Ala
      105                      110                      115
agg aaa tct aat ttc agc ctc gag gac ttc cag cac agc aaa ggc aag      639
Arg Lys Ser Asn Phe Ser Leu Glu Asp Phe Gln His Ser Lys Gly Lys
      120                      125                      130                      135
gaa ccc tac agc tct tcc aaa tat gcc act gac ctt ttg agt gtg gct      687
Glu Pro Tyr Ser Ser Ser Lys Tyr Ala Thr Asp Leu Leu Ser Val Ala
      140                      145                      150
ttg aac agg aac ttc aac cag cag ggt ctc tat tcc aat gtg gcc tgt      735
Leu Asn Arg Asn Phe Asn Gln Gln Gly Leu Tyr Ser Asn Val Ala Cys
      155                      160                      165
cca ggt aca gca ttg acc aat ttg aca tat gga att ctg cct ccg ttt      783
Pro Gly Thr Ala Leu Thr Asn Leu Thr Tyr Gly Ile Leu Pro Pro Phe
      170                      175                      180
ata tgg acg ctg ttg atg ccg gca ata ttg cta ctt cgc ttt ttt gca      831
Ile Trp Thr Leu Leu Met Pro Ala Ile Leu Leu Leu Arg Phe Phe Ala
      185                      190                      195
aat gca ttc act ttg aca cca tat aat gga aca gaa gct ctg gta tgg      879
Asn Ala Phe Thr Leu Thr Pro Tyr Asn Gly Thr Glu Ala Leu Val Trp
      200                      205                      210                      215
ctt ttc cac caa aag cct gaa tct ctc aat cct ctg atc aaa tat ctg      927
Leu Phe His Gln Lys Pro Glu Ser Leu Asn Pro Leu Ile Lys Tyr Leu
      220                      225                      230
agt gcc acc act ggc ttt gga aga aat tac att atg acc cag aag atg      975
Ser Ala Thr Thr Gly Phe Gly Arg Asn Tyr Ile Met Thr Gln Lys Met
      235                      240                      245
gac cta gat gaa gac act gct gaa aaa ttt tat caa aag tta ctg gaa      1023
Asp Leu Asp Glu Asp Thr Ala Glu Lys Phe Tyr Gln Lys Leu Leu Glu
      250                      255                      260
ctg gaa aag cac att agg gtc act att caa aaa aca gat aat cag gcc      1071
Leu Glu Lys His Ile Arg Val Thr Ile Gln Lys Thr Asp Asn Gln Ala
      265                      270                      275
agg ctc agt ggc tca tgc cta taattccagc actttgggag gccaaaggcag      1122
Arg Leu Ser Gly Ser Cys Leu
      280                      285
aaggatcact tgagaccagg agttcaagac cagcctgaga aacatagtga gcccttgtct      1182
ctacaaaaag aaataaaaaat aatagctggg tgtggtggca tgcgcatgta gtcccagcta      1242
ctcagaagga tgaggtggga ggatctcttg aggctgggag gcagaggttg cagtgaagctg      1302
agattgtgcc actgcactcc agcctgggtg acagcgagac cctgtctcaa aatatgtata      1362
tatttaatat atatataaaa ccagagctga caatgacact ctggaacatt gcataccttc      1422
tgtacattct ggggtacatg gatttctact gagttggata atatgcattt gtaataaaact      1482
atgaactatg aaaaaaaaaa aa                                          1504

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<210> 372

<211> 765

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 274..597

<221> sig_peptide

<222> 274..399

<223> Von Heijne matrix

score 5.19999980926514

seq LLFDLVCHEFCQS/DD

<221> polyA_signal

<222> 731..736

<221> polyA_site

<222> 754..765

<400> 372

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accaggaaca tccagctatt tatgatagca tttgcttcat tatgtcaagt tcaacaaatg      60
ttgacttgct ggtgaagggtg ggggaggttg tggacaagct ctttgatttg gatgagaaac      120
taatgttaag aatgggtcag aaatggggct gctcagcctc tggaccaacc ccaggaagag      180
tctgaagagc agccagtgtt tcggcttctg ccctgtatac ttgaagctgc caaacaagta      240
cgttctgaaa atccagaatg gcttgatggt tac atg cac att tta caa ctg ctt      294
                               Met His Ile Leu Gln Leu Leu
                               -40
act aca gtg gat gat gga att caa gca att gta cat tgt cct gac act      342
Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His Cys Pro Asp Thr
-35                               -30                               -25                               -20
gga aaa gac att tgg aat tta ctt ttt gac ctg gtc tgc cat gaa ttc      390
Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val Cys His Glu Phe
                               -15                               -10                               -5
tgc cag tct gat gat cca gcc atc att ctt caa raa car aaa acr gtg      438
Cys Gln Ser Asp Asp Pro Ala Ile Ile Leu Gln Xaa Gln Lys Thr Val
                               1                               5                               10
cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat gcc tca cag act      486
Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr Ala Ser Gln Thr
                               15                               20                               25
gag caa gak tat cta aar ata raa aaa gga gac ggt ggc tca ggg agt      534
Glu Gln Xaa Tyr Leu Lys Ile Xaa Lys Gly Asp Gly Gly Ser Gly Ser
                               30                               35                               40                               45
aaa gga agg cca ktt gan caa aca gaa ktg ttc ctc tgc att tca aaa      582
Lys Gly Arg Pro Xaa Xaa Gln Thr Glu Xaa Phe Leu Cys Ile Ser Lys
                               50                               55                               60
cct tct tcc ttt cta tagccctgtg gtggaagatt ttattaaaaat cctacgtgaa      637
Pro Ser Ser Phe Leu
                               65
gttgataagg cgcttgctga tgacttgga aaaaacttcc caagtttgaa ggttcagact      697
taaaacctga attggaatta cttctgtaca agaaataaac tttatttttc tcaactgacaa      757
aaaaaaaaa                                                                765

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<210> 373

<211> 1041

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 230..469

<221> sig_peptide

<222> 230..307

<223> Von Heijne matrix
 score 4.90000009536743
 seq VLCTNQVLITARA/VP

<221> polyA_signal

<222> 1004..1009

<221> polyA_site

<222> 1027..1040

<400> 373

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aacttccaag ttgtagtggt gttgttttca gcctgctgct gctgctgcta ttgctgctag      60
gggaaccgctc gtggggaagg atggtgtgctg aaaaatgtga aaagaaactt ggtactgtta      120
tcaactccaga tacatggaaa gatggtgcta ggaataccac agaaagtggg ggaagaaagc      180
tgaatgaaaaa taaagctttg acttcaaaaaa aagccagaat tgatccata atg gaa gaa      238
                                   Met Glu Glu
                                   -25
ata agt tct cca ctt gta gaa ttt gta aaa gtt ttg tgc acc aac cag      286
Ile Ser Ser Pro Leu Val Glu Phe Val Lys Val Leu Cys Thr Asn Gln
                                   -20      -15      -10
gtt ctc att act gcc agg gct gtg cct aca aaa aag gca tct gtg cga      334
Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala Ser Val Arg
                                   -5      1      5
tgt gtg gaa aaa agg ttt tgg ata cca aaa act aca agc aaa cat ctg      382
Cys Val Glu Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser Lys His Leu
10      15      20      25
tct aga tgt att gat gga att tct ggc ttt cta aat gat ttt act ttc      430
Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp Phe Thr Phe
                                   30      35      40
tgc ctt gaa ttt tca agg cat aga tgt caa ctt aca gaa taacatgkt      479
Cys Leu Glu Phe Ser Arg His Arg Cys Gln Leu Thr Glu
                                   45      50
taagataatt aagtktaaac cagaraattt gattgttact cattttgctc tcatgktcta      539
aaacagcaac agtgtaacta gtcttttggt gttaatgggt attttcctta taaaaatttt      599
aaaaaactaag tggcaaattc catgaaaata tttctcagtt ctgtatgcac ttttatttaa      659
cattattcat ataattctcc cccaccact ttatttataa atactgcaaa aktgaraagg      719
agataataaa tactttgctc tgaatttggc atccaaagtt aacatttctc cctcactcc      779
cttgctgggtg tcatagttat tagaatcagc agcctcttaa ctaattgcgg tttcatagga      839
tatataaatg tttcaagcca ttattgctga atggttcttt agttattaac ctagacccaa      899
atcaaagacc agttggattt atgatatttt ttatttggtt ttgcagccaa agtgccagtt      959
tctttaatat gtgaccaaga acacaaggag catccatatg gccaaataaa tacactgaat      1019
tttagaaaaa caaaaaaaaaa ar      1041

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<210> 374

<211> 1164

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 72..545

<221> sig_peptide

<222> 72..203

<223> Von Heijne matrix

score 5.5

seq ILFFTGWWIMIDA/AV

<221> polyA_site

<222> 1151..1162

<400> 374

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aaagtcggcg tggacgtttg aggaagctgg gatacagcat ttaatgaaaa atttatgctt      60
aagaagtaaa a atg gca ggc ttc cta gat aat ttt cgt tgg cca gaa tgt      110
                                   Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys
                                   -40      -35
gaa tgt att gac tgg agt gag aga aga aat gct gtg gca tct gtt gtc      158
Glu Cys Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val

```

```

      -30      -25      -20
gca ggt ata ttg ttt ttt aca ggc tgg tgg ata atg att gat gca gct      206
Ala Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
-15      -10      -5      1
gtg gtg tat cct aag cca gaa cag ttg aac cat gcc ttt cac aca tgt      254
Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr Cys
      5      10      15
ggt gta ttt tcc aca ttg gct ttc ttc atg ata aat gct gta tcc aat      302
Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val Ser Asn
      20      25      30
gct cag gtg aga ggt gat agc tat gaa agc ggc tgt tta gga aga aca      350
Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu Gly Arg Thr
      35      40      45
ggt gct cga gtt tgg ctt ttc att ggt ttc atg ttg atg ttt ggg tca      398
Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu Met Phe Gly Ser
50      55      60      65
ctt att gct tcc atg tgg att ctt ttt ggt gca tat gtt acc caa aat      446
Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala Tyr Val Thr Gln Asn
      70      75      80
act gat gtt tat ccg gga cta gct gtg ttt ttt caa aat gca ctt ata      494
Thr Asp Val Tyr Pro Gly Leu Ala Val Phe Phe Gln Asn Ala Leu Ile
      85      90      95
ttt ttt agc act ctg atc tac aaa ttt gga aga acc gaa gag cta tgg      542
Phe Phe Ser Thr Leu Ile Tyr Lys Phe Gly Arg Thr Glu Glu Leu Trp
      100      105      110
acc tgagatcact tcttaagtca cattttcctt ttgttatatt ctgtttgtag      595
Thr
ataggttttt tatctctcag tacacattgc caaatggagt agattgtaca ttaaattgttt      655
tgtttcttta catttttatg ttctgagttt tgaaatagtt ttatgaaatt tctttatttt      715
tcattgcata gactgttaat atgtatataa tacaagacta tatgaattgg ataatgagta      775
tcagtttttt attcctgaga tttagaactt gatctactcc ctgagccagg gttacatcat      835
cttgctcatt tagaagtaac cactcttgct tctctggctg ggcaagggtg ctcatgcctg      895
taatcccagc actttgggag gccgaggcgg gccgattgct tgaggtcaag tgtttgagac      955
cagcctggcc aacatggcga aaccccatct actaaaaata caaaaattag ccaggcatgg      1015
tggtgggtgc ctgtaatccc aactacctag gaggtgagg caggagaatc gcttgaaccc      1075
ggggggcaga ggttgyagtg agctgagttt gcgccactgc actctagcct gggggagaaa      1135
gtgaaactcc ctctcaaaaa aaaaaaamc      1164

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<210> 375

<211> 1250

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 36..425

<221> sig_peptide

<222> 36..119

<223> Von Heijne matrix

score 11.6000003814697

seq LLLLVQLLRFLRA/DG

<221> polyA_signal

<222> 1215..1220

<221> polyA_site

<222> 1240..1250

<400> 375

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atttcttccc cccgagctgg gcgtgcgcgg ccgca atg aac tgg gag ctg ctg      53
                               Met Asn Trp Glu Leu Leu
                               -25
ctg tgg ctg ctg gtg ctg tgc gcg ctg ctc ctg ctc ttg gtg cag ctg      101
Leu Trp Leu Leu Val Leu Cys Ala Leu Leu Leu Leu Val Gln Leu
-20 -15 -10
ctg cgc ttc ctg agg gct gac ggc gac ctg acg cta cta tgg gcc gag      149
Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu Thr Leu Leu Trp Ala Glu
-5 1 5 10
tgg cag gga cga cgc cca gaa tgg gag ctg act gat atg gtg gtg tgg      197
Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu Thr Asp Met Val Val Trp
15 20 25
gtg act gga gcc tcg agt gga att ggt gag gag ctg gct tac cag ttg      245
Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu Leu Ala Tyr Gln Leu
30 35 40
tct aaa cta gga gtt tct ctt gtg ctg tca gcc aga aga gtg cat gag      293
Ser Lys Leu Gly Val Ser Leu Val Leu Ser Ala Arg Arg Val His Glu
45 50 55
ctg gaa agg gtg aaa aga aga tgc cta gag aat ggc aat tta aaa gaa      341
Leu Glu Arg Val Lys Arg Arg Cys Leu Glu Asn Gly Asn Leu Lys Glu
60 65 70
aaa gat ata ctt gtt ttg ccc ctt gac ctg acc gac act ggt tcc cat      389
Lys Asp Ile Leu Val Leu Pro Leu Asp Leu Thr Asp Thr Gly Ser His
75 80 85 90
gaa agc ggc tac caa agc tgt tct cca gga att tgg tagaatcgac      435
Glu Ser Gly Tyr Gln Ser Cys Ser Pro Gly Ile Trp
95 100
attctgtgtca acaatgtgga aatgtccag cgttctctgt gcatggatac caacttggat      495
gtctacagaa agctaagtga agcttaacta cttagggacg gtgtccttga caaaatgtgk      555
kctgcctcac atgacgaga ngaarcaaagg aaagattgtt actgtgaata gcatcctggg      615
tatcatatct gtacctctt ccattggata ctgtgctagc aagcatgctc tccggggkktk      675
ktttaatggc cttcraacag aacttgccac ataccargt ataatagttt ctaacatttg      735
cccaggacct gtgcaatcaa atattgtgga aaattcccta gctggagaag tcacaaagac      795
tataggcaat aatggagacc agtcccacaa gatgacaacc agtcgttgtg tgcggctgat      855
gttaatcagc atggccaatg atttgaaaga agtttggatc tcagaacaac ctttcttgtt      915
agtaacatat ttgtggcaat acatgccaac ctgggcctgg tggataacca acaagatggg      975
gaagaaaagg attgagaact ttaagagtgg tgtggatgca gactcttctt attttaaaat      1035
ctttaagaca aaacatgact gaaaagagca cctgtacttt tcaagccact ggagggagaa      1095
atggaaaaca tgaacacagc aatcttctta tgcttctgaa taatcaaaga ctaatttgtg      1155
attttacttt ttaatagata tgactttgct tccaacatgg aatgaaataa aaaataaata      1215
ataaaaagatt gccatgaatc ttgcaaaaaa aaaaa      1250

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<210> 376

<211> 947

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 155..751

<221> sig_peptide

<222> 155..340

<223> Von Heijne matrix

score 3.70000004768372

seq SILGIISVPLSIG/YC

<221> polyA_signal

<222> 912..917

<221> polyA_site

<222> 937..947

<400> 376

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agtgaaaaga agatgcctag agaatggcaa tttaaaagaa aaagatatatc ttgttttgcc      60
ccttgacctg accgacctg gttcccatga agcggctacc aaagctgttc tccaggagtt      120
tggtagaatc gacattctgg tcaacaatgg tgga atg tcc cag cgt tct ctg tgc      175
                               Met Ser Gln Arg Ser Leu Cys
                               -60
atg gat acc agc ttg gat gtc tac aga rag cta ata gag ctt aac tac      223
Met Asp Thr Ser Leu Asp Val Tyr Arg Xaa Leu Ile Glu Leu Asn Tyr
-55                               -50                               -45                               -40
tta ggg acg gtg tcc ttg aca aaa tgt gtt ctg cct cac atg atc gag      271
Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His Met Ile Glu
                               -35                               -30                               -25
agg aag caa gga aag att gtt act gtg aat agc atc ctg ggt atc ata      319
Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu Gly Ile Ile
                               -20                               -15                               -10
tct gta cct ctt tcc att gga tac tgt gct agc aag cat gct ctc cgg      367
Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His Ala Leu Arg
                               -5                               1                               5
ggg ttt ttt aat ggc ctt cga aca gaa ctt gcc aca tac cca ggt ata      415
Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly Ile
10                               15                               20                               25
ata gtt tct aac att tgc cca gga cct gtg caa tca aat att gtg gaa      463
Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val Glu
                               30                               35                               40
aat tcc cta gct gga gaa gtc aca aaa act ata ggc aat aat gga aac      511
Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly Asn
                               45                               50                               55
cag tcc cac aag atg aca acc agt cgt tgt gtg cgg ctg atg tta atc      559
Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu Ile
                               60                               65                               70
agc atg gcc aat gat ttg aaa gaa gtt tgg atc tca gaa caa cct ttc      607
Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro Phe
75                               80                               85
ttg tta gta aca tat ttg tgg caa tac atg cca acc tgg gcc tgg tgg      655
Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala Trp Trp
90                               95                               100                               105
ata acc aac aag atg ggg aag aaa agg att gag aac ttt aag agt ggt      703
Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe Lys Ser Gly
                               110                               115                               120
gtg gat gcm rac tct tct tat ttt aaa atc ttt aag aca aaa cat gac      751
Val Asp Ala Xaa Ser Ser Tyr Phe Lys Ile Phe Lys Thr Lys His Asp
                               125                               130                               135
tgaaaaganc acctgtactt ttcaagccac tggagggaga aatggaaaac atgaaaacag      811
caatcttctt atgcttctga ataatacaag actaatttgt gattttactt tttaatagat      871
atgactttgc ttccaacatg grrtgaaata aaaaataaat aataaaaagat tgccatgrrt      931
cttgcaaaaa aaaaaa                                         947

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<210> 377

<211> 621

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 46..585

<221> sig_peptide

<222> 46..120

<223> Von Heijne matrix
 score 6.30000019073486
 seq AFSLSVMAALTFG/CF

<221> polyA_signal

<222> 584..589

<221> polyA_site

<222> 606..619

<400> 377

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aactgggtgt gcgtrtggag tccggactcg tgggagacga tcgctg atg aac acg gtg      57
                                     Met Asn Thr Val
                                     -25
ctg tcg cgg gcg aac tca ctg ttc gcc ttc tcg ctg agc gtg atg gcs      105
Leu Ser Arg Ala Asn Ser Leu Phe Ala Phe Ser Leu Ser Val Met Ala
-20                               -15                               -10
gcg ctc acc ttc ggc tgc ttc atc ayy acc gcc ttc aaa gac agg agc      153
Ala Leu Thr Phe Gly Cys Phe Ile Xaa Thr Ala Phe Lys Asp Arg Ser
-5                               1                               5                               10
gtc ccg gtg cgg ctg cac gtc tcg cga atc atg cta aaa aat gta gaa      201
Val Pro Val Arg Leu His Val Ser Arg Ile Met Leu Lys Asn Val Glu
15                               20                               25
gat ttc act gga cct aga gaa aga agt gat ctg gga ttt atc aca ttt      249
Asp Phe Thr Gly Pro Arg Glu Arg Ser Asp Leu Gly Phe Ile Thr Phe
30                               35                               40
gat ata act gct gat cta gag aat ata ttt gat tgg aat gtt aag cag      297
Asp Ile Thr Ala Asp Leu Glu Asn Ile Phe Asp Trp Asn Val Lys Gln
45                               50                               55
ttg ttt ctt tat tta tca gca gaa tat tca aca aaa aat aat gct ctg      345
Leu Phe Leu Tyr Leu Ser Ala Glu Tyr Ser Thr Lys Asn Asn Ala Leu
60                               65                               70                               75
aac caa ktt gtc cta tgg gac aag att gtt ttg aga ggt gat aat ccg      393
Asn Gln Xaa Val Leu Trp Asp Lys Ile Val Leu Arg Gly Asp Asn Pro
80                               85                               90
aag ctg ctg ctg aaa gat atg aaa aca aaa tat ttt ttc ttt gac gat      441
Lys Leu Leu Leu Lys Asp Met Lys Thr Lys Tyr Phe Phe Phe Asp Asp
95                               100                               105
gga aat ggt ctc wag gga aac agg aat gtc act ttg acc ctg tct tgg      489
Gly Asn Gly Leu Xaa Gly Asn Arg Asn Val Thr Leu Thr Leu Ser Trp
110                               115                               120
aac gtc gta cca aat gct gga att cta cct ctt gtg aca gga tca gga      537
Asn Val Val Pro Asn Ala Gly Ile Leu Pro Leu Val Thr Gly Ser Gly
125                               130                               135
cac gta tct gtc cca ttt cca gat aca tat gaa ata acg aag agt tat      585
His Val Ser Val Pro Phe Pro Asp Thr Tyr Glu Ile Thr Lys Ser Tyr
140                               145                               150                               155
taaattattc tgaatttgaa acaaaaaaaaaaaaahm      621

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<210> 378

<211> 52

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<400> 378

Met Pro Ser Val Asn Ser Ala Gly Leu Cys Val Leu Gln Leu Thr Thr
 -20 -15 -10 -5
 Ala Val Thr Ser Ala Phe Leu Leu Ala Lys Val Asn Pro Phe Glu Xaa
 1 5 10
 Phe Leu Ser Arg Gly Phe Trp Leu Cys Ala Ala His His Phe Ile His
 15 20 25
 Pro Cys Leu Asp
 30

<210> 379
 <211> 193
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 379
 Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu Pro Pro Leu Xaa
 -20 -15 -10
 Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro Glu Arg Gly Ala
 -5 1 5
 Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg Phe Cys Pro Pro
 10 15 20 25
 Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp Lys Tyr Ser Asn
 30 35 40
 Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu Ser Pro Leu Glu
 45 50 55
 Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu Trp Asn Gln Gln
 60 65 70
 Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu Lys Glu Glu Phe
 75 80 85
 Ile His Ser Arg Leu Lys Thr Lys Gly Leu Gly Leu Arg Thr Glu Ser
 90 95 100 105
 Gly Gln Lys Ala Thr Leu Asn Ala Glu Glu Met Ala Asp Phe Tyr Lys
 110 115 120
 Glu Phe Leu Ser Lys Asn Phe Gln Lys His Met Tyr Tyr Asn Arg Asp
 125 130 135
 Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met Gly Lys Val Ala
 140 145 150
 Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln Lys Lys Arg Ser
 155 160 165
 Asn
 170

<210> 380
 <211> 82
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 380
 Met Ala Phe Thr Leu Xaa Ser Leu Leu Gln Ala Ala Leu Leu Cys Val
 -10 -5 1

Asn Ala Ile Ala Val Leu His Glu Glu Arg Phe Leu Lys Asn Ile Gly
 5 10 15
 Trp Gly Thr Asp Gln Gly Ile Gly Gly Phe Gly Glu Glu Pro Gly Ile
 20 25 30
 Lys Ser Xaa Xaa Met Xaa Leu Ile Arg Ser Val Arg Thr Val Met Arg
 35 40 45 50
 Val Pro Leu Ile Ile Val Asn Ser Ile Ala Ile Val Leu Leu Leu Leu
 55 60 65
 Phe Gly

<210> 381
 <211> 198
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 381
 Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val Thr
 -20 -15 -10
 Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala Gln His
 -5 1 5 10
 Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu Gly Gln Ala
 15 20 25
 Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg Leu Thr Lys Ala Arg
 30 35 40
 Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu Leu Leu Gly Gln Glu
 45 50 55
 Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu Arg Ala Ser Leu Leu
 60 65 70 75
 Glu Thr Gln Met Glu Glu Asp Ile Leu Xaa Leu Gln Ala Xaa Ala Thr
 80 85 90
 Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln Lys Val Leu Arg Asp
 95 100 105
 Ser Val Gln Arg Leu Xaa Xaa Gln Leu Xaa Xaa Ala Trp Leu Gly Pro
 110 115 120
 Ala Tyr Arg Lys Phe Glu Val Leu Lys Ala Pro Pro Xaa Lys Gln Asn
 125 130 135
 His Ile Leu Trp Ala Leu Thr Gly His Val Xaa Arg Gln Xaa Arg Glu
 140 145 150 155
 Met Val Ala Gln Gln Xaa Xaa Leu Xaa Gln Ile Gln Glu Lys Leu His
 160 165 170
 Thr Ala Ala Leu Pro Ala
 175

<210> 382
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55...-1

<400> 382
 Met Asp Lys Leu Lys Lys Val Leu Ser Gly Gln Asp Thr Glu Asp Arg

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-55          -50          -45          -40
Ser Gly Leu Ser Glu Val Val Glu Ala Ser Ser Leu Ser Trp Ser Thr
          -35          -30          -25
Arg Ile Lys Gly Phe Ile Ala Cys Phe Ala Ile Gly Ile Leu Cys Ser
          -20          -15          -10
Leu Leu Gly Thr Val Leu Leu Trp Val Pro Arg Lys Gly Leu His Leu
          -5          1          5
Phe Ala Val Phe Tyr Thr Phe Gly Asn Ile Ala Ser Ile Gly Ser Thr
10          15          20          25
Ile Phe Leu Met Gly Pro Val Lys Gln Leu Lys Arg Met Phe Glu Pro
          30          35          40
Thr Arg Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr
          45          50          55
Leu Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe
          60          65          70
Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe Ile
          75          80          85
Pro Phe Ala Arg Asp Ala Val Lys Xaa Cys Phe Ala Val Cys Leu Ala
90          95          100          105

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<210> 383
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

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<400> 383
Met Lys Ala Leu Cys Leu Leu Leu Leu Pro Val Leu Gly Leu Leu Val
          -15          -10          -5
Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile Asn Glu Arg Ile
          1          5          10
Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile Ser Ser Ile Gly
15          20          25          30
Arg Gly Ser Glu Ser Val Thr Ser Arg Gly Asp Leu Ala Thr Cys Pro
          35          40          45
Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser Ala Cys Gly Ser
          50          55          60
Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln Cys Ala Gly Met
          65          70          75
Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
          80          85          90

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<210> 384
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

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<400> 384
Met Ile Ser Arg Gln Leu Arg Ser Leu Ser Cys Leu Cys Pro Ala Leu
          -20          -15          -10
Phe Pro Gly Thr Ser Ser Phe Ile Val Ala Leu Ser Ser Pro Ala Asp

```

```

      -5              1              5              10
Leu Tyr Ile Pro Xaa Arg Xaa Arg Ser Asp Glu Leu Val Phe Glu Ser
      15              20              25
Gln Lys Gly Ser Ala Met Glu Leu Ala Val Ile Thr Val Xaa Gly Val
      30              35              40

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<210> 385
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

```

<400> 385
Met Gly Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser
-15              -10              -5              1
Ala Lys Pro Asn Glu Gln Pro Trp Leu Leu Asn
      5              10

```

<210> 386
 <211> 186
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

```

<400> 386
Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile
-20              -15              -10
Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser
-5              1              5              10
Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp
      15              20              25
Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro
      30              35              40
Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly
      45              50              55
Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr His Xaa Ser Xaa Lys
      60              65              70              75
Ala Ala His Pro Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser
      80              85              90
Pro Ser Thr Xaa Val His Xaa Arg Pro Xaa Xaa Pro Ser Xaa His Leu
      95              100              105
Val Phe Met Arg Met Thr Pro Ser Ser Met Met Asn Thr Pro Ser Gly
      110              115              120
Asn Xaa Gly Cys Trp Ser Gln Leu Cys Cys Ser Ser Gln Ala Ser Ser
      125              130              135
Ser Ser Pro Val Ala Ser Ala Gly Ser Cys Pro Gly Tyr Ala Gly Ile
      140              145              150              155
Ile Ala Gly Glu Ser Ile Arg Asn Arg Ser
      160              165

```

```
<210> 387
<211> 179
<212> PRT
<213> Homo sapiens
```

```

<220>
<221> SIGNAL
<222> -26..-1

```

[illegible]

```
<210> 388
<211> 150
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -55..-1
```

```

<400> 388
Met Ala Thr Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys
-55 -50 -45 -40
Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu
-35 -30 -25
Thr Val Ala Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr
-20 -15 -10
Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met
-5 1 5
Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly
10 15 20 25
Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr
30 35 40
Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu
45 50 55
Leu Ala His Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Ala
60 65 70

```

Pro Phe Pro Val Gly Asp Ser Gly Ser Gly Arg Gly Leu Gln Pro Ser
 75 80 85
 Pro Gly Cys Tyr Arg Tyr
 90 95

<210> 389
 <211> 236
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 389
 Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys
 -30 -25 -20
 Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Ala Ala
 -15 -10 -5 1
 Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
 5 10 15
 Ser Val Leu Lys Leu His His Ser Leu Gln Xaa Ser Xaa Pro Asp Leu
 20 25 30
 Arg His Leu Val Leu Val Xaa Asn Thr Leu Arg Arg Ile Gln Ala Ser
 35 40 45
 Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Thr Pro Pro Ala Ala
 50 55 60 65
 Pro Xaa Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser
 70 75 80
 Ala Ser Met Ala Xaa Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu
 85 90 95
 Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser
 100 105 110
 Ile Gly Gly Xaa Pro Pro Xaa Leu Gly Ala Leu Asp Leu Leu Gly Pro
 115 120 125
 Ala Thr Gly Cys Leu Leu Asp Asn Gly Leu Glu Gly Leu Phe Glu Asp
 130 135 140 145
 Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu
 150 155 160
 Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro
 165 170 175
 Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly
 180 185 190
 Thr Gln Ala Leu Glu Arg Pro Pro Gly Pro Gly Arg
 195 200 205

<210> 390
 <211> 149
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -100...-1

<400> 390
 Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
 -100 -95 -90 -85

[illegible]

```
<210> 391
<211> 69
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -49..-1
```

```

<400> 391
Met Pro Phe His Phe Pro Phe Leu Gly Phe Val Cys Leu His Leu His
          -45                      -40                      -35
Leu Thr Pro Cys Leu Thr Val Pro Arg Arg Pro Leu Phe Leu Leu Leu
          -30                      -25                      -20
His Leu Cys Pro His Leu Pro Phe Leu Leu Leu Leu Ser Cys Val Gly
          -15                      -10                      -5
Xaa Xaa Pro Ser Cys Leu Pro Ser Ser Ser Thr Cys Val Ser Leu His
  1          5          10
Phe Phe Ile Pro Asp
          20

```

```
<210> 392
<211> 241
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -30..-1
```

```

<400> 392
Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu Gln Thr Asn
-30                -25                -20                -15
Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr Leu Ser Val
                -10                -5                1
Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu Ala Val Thr
        5                10                15
Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu Gln Pro Thr
        20                25                30

```

Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn Leu Cys Leu
 35 40 45 50
 Asp Gly Cys Lys Ser Glu Ala Xaa Lys Phe Thr Val Arg Glu Ala Leu
 55 60 65
 Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr Ser Asn Asp
 70 75 80
 Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val Pro Glu Ala
 85 90 95
 Arg Ala Lys Gln Thr Gly Gly Gly Thr Thr Leu Val Val Arg Glu Ile
 100 105 110
 Lys Leu Leu Ser Lys Glu Leu Arg Ser Phe Leu Thr Ala Leu Val Ser
 115 120 125 130
 Leu Leu Ser Val Tyr Val Thr Gly Val Cys Val Ala Phe Ile Leu Leu
 135 140 145
 Ser Lys Ser Lys Ser Asn Pro Leu Arg Asn Lys Glu Ile Lys Glu Asp
 150 155 160
 Ser Gln Lys Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu Ile Ala Gln
 165 170 175
 Glu Leu Tyr His Lys Arg His Val Glu Thr Asn Gln Gln Ser Glu Lys
 180 185 190
 Asp Asn Asn Thr Tyr Glu Asn Arg Arg Val Leu Ser Asn Tyr Glu Arg
 195 200 205 210
 Pro

<210> 393

<211> 47

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -30...-1

<400> 393

Met Asn Cys Asn Val Val Ser Glu Arg Gly Lys Trp Leu Glu Val Glu
 -30 -25 -20 -15
 Cys Ser Leu Met Thr Cys Thr Thr Leu Ile Asn Ala Ser Ala Ile Ser
 -10 -5 1
 Thr Asn Thr Leu Thr Asp Met Gly Ser Phe Asp Arg Arg Glu Ser
 5 10 15

<210> 394

<211> 65

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 394

Met Ala Phe Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro
 -25 -20 -15
 Leu Gln Trp Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser
 -10 -5 1
 Tyr Gly Val Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu
 5 10 15 20
 Phe Leu Glu Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Xaa

Ser 25 30 35

<210> 395
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 395
 Met Thr Cys Trp Met Leu Pro Pro Ile Ser Phe Leu Ser Tyr Leu Pro
 -20 -15 -10
 Leu Trp Leu Gly Pro Ile Trp Pro Cys Ser Gly Ser Thr Leu Gly Lys
 -5 1 5
 Pro Asp Pro Gly Val Trp Pro Ser Leu Phe Arg Pro Trp Asp Ala Ala
 10 15 20
 Ser Pro Gly Asn Tyr Ala Leu Ser Arg Gly Xaa Asn Xaa Tyr Xaa Xaa
 25 30 35 40
 Trp Gly Gln Gly Thr His Ser Ser Leu
 45

<210> 396
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 396
 Met Pro Cys Pro Thr Trp Thr Cys Leu Lys Ser Phe Pro Ser Pro Thr
 -15 -10 -5
 Ser Ser His Ala Ser Ser Leu His Leu Pro Pro Ser Cys Thr Arg Leu
 1 5 10
 Thr Leu Thr Gln Thr Leu Arg Thr Gly Met His Leu Ser Arg Ala Leu
 15 20 25 30
 Gln Gly Thr Leu Thr Arg Leu Gln Ser Thr Pro Ala
 35 40

<210> 397
 <211> 192
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -93...-1

<400> 397
 Met Ala Glu Leu Gly Leu Asn Glu His His Gln Asn Glu Val Ile Asn
 -90 -85 -80
 Tyr Met Arg Phe Ala Arg Ser Lys Arg Gly Leu Arg Leu Lys Thr Val


```

      -75      -70      -65
Asp Ser Cys Phe Gln Asp Leu Lys Glu Ser Arg Leu Val Glu Asp Thr
      -60      -55      -50
Phe Thr Ile Asp Glu Val Ser Glu Val Leu Asn Gly Leu Gln Ala Val
      -45      -40      -35      -30
Val His Ser Glu Val Glu Ser Glu Leu Ile Asn Thr Ala Tyr Thr Asn
      -25      -20      -15
Val Leu Leu Leu Arg Gln Leu Phe Ala Gln Ala Glu Lys Trp Tyr Leu
      -10      -5      1
Lys Leu Gln Thr Asp Ile Ser Glu Leu Glu Asn Arg Glu Leu Leu Glu
      5      10      15
Gln Xaa Ala Glu Phe Glu Lys Ala Xaa Ile Thr Ser Ser Asn Lys Lys
      20      25      30      35
Pro Ile Leu Xaa Val Thr Xaa Pro Lys Leu Ala Pro Leu Asn Glu Gly
      40      45      50
Gly Thr Ala Lys Leu Leu Asn Lys Val Ile Cys Ile Ile Leu Arg Asn
      55      60      65
Gly Lys Ser Leu Ile Leu Ser Cys His Cys Leu Gly Trp Arg Asn Lys
      70      75      80
Ser Gly Arg Phe Val Ser Gly Pro Leu Arg Ile Ile Ser Pro Leu Gln
      85      90      95

```

<210> 398
 <211> 149
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -72...-1

```

<400> 398
Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr Ile Ser Ile Phe
      -70      -65      -60
Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro Ile Gln Ala Leu
      -55      -50      -45
Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln Lys
      -40      -35      -30      -25
Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu Ala
      -20      -15      -10
Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His Ala
      -5      1      5
Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg Met Glu Ser Val
      10      15      20
Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala Pro Gly Pro Tyr
      25      30      35      40
Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro Val Ala Pro Gln
      45      50      55
His Thr Leu Lys Leu Ile Thr Tyr Val Lys Lys Asn Gln Lys Thr Leu
      60      65      70
Phe Ser Met Val Gly
      75

```

<210> 399
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 399
 Met Thr Pro Leu Leu Thr Leu Ile Leu Val Val Leu Met Gly Leu Pro
 -20 -15 -10 -5
 Leu Ala Gln Ala Leu Asp Cys His Val Cys Ala Tyr Asn Gly Asp Asn
 1 5 10
 Cys Phe Asn Pro Met Arg Cys Pro Ala Met Val Ala Tyr Cys Met Thr
 15 20 25
 Thr Arg Thr Tyr Tyr Thr Pro Thr Arg Met Lys Val Ser Lys Ser Cys
 30 35 40
 Val Pro Arg Cys Phe Glu Xaa Cys Val
 45 50

<210> 400
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 400
 Met Asn Leu His Phe Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly
 -20 -15 -10 -5
 Leu Val Leu Ala Pro Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe
 1 5 10
 Pro Cys Ile Tyr Cys Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala
 15 20 25
 Phe Ser Phe Ile Thr Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu
 30 35 40
 Ile Leu Pro Glu Lys Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly
 45 50 55 60
 Pro Xaa Lys Leu Arg Gln
 65

<210> 401
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 401
 Met Cys Pro Val Phe Ser Lys Gln Leu Leu Ala Cys Gly Ser Leu Leu
 -20 -15 -10
 Pro Gly Leu Trp Gln His Leu Thr Ala Asn His Trp Pro Pro Phe Ser
 -5 1 5 10
 Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser Glu Gln Ile Ser Glu
 15 20 25
 Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Arg Ser Leu Asn Gln Glu
 30 35 40
 Pro Phe Val Ser Arg Ala Ile Arg Pro Lys Tyr Ser Ile Thr

45

50

55

<210> 402
 <211> 65
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 402
 Met Gly Lys Gly His Gln Arg Pro Trp Trp Lys Val Leu Pro Leu Ser
 -25 -20 -15
 Cys Phe Leu Val Ala Leu Ile Ile Trp Cys Tyr Leu Arg Glu Glu Ser
 -10 -5 1
 Glu Ala Asp Gln Trp Leu Arg Gln Val Trp Gly Glu Val Pro Glu Pro
 5 10 15 20
 Ser Asp Arg Ser Glu Glu Pro Glu Thr Pro Ala Ala Tyr Arg Ala Arg
 25 30 35
 Thr

<210> 403
 <211> 211
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 403
 Met Leu Leu Leu Ser Ile Thr Thr Ala Tyr Thr Gly Leu Glu Leu Thr
 -25 -20 -15
 Phe Phe Ser Gly Val Tyr Gly Thr Cys Ile Gly Ala Thr Asn Lys Phe
 -10 -5 1 5
 Gly Ala Glu Glu Xaa Ser Leu Ile Gly Leu Ser Gly Ile Phe Ile Gly
 10 15 20
 Ile Gly Glu Ile Leu Gly Gly Ser Leu Phe Gly Leu Leu Ser Lys Asn
 25 30 35
 Asn Arg Phe Gly Arg Asn Pro Val Val Leu Leu Gly Ile Leu Val His
 40 45 50
 Phe Ile Ala Phe Tyr Leu Ile Phe Leu Asn Met Pro Gly Asp Ala Pro
 55 60 65
 Ile Ala Pro Val Lys Gly Thr Asp Ser Ser Ala Tyr Ile Lys Ser Ser
 70 75 80 85
 Lys Xaa Phe Ala Ile Leu Cys Xaa Phe Leu Xaa Gly Leu Gly Asn Ser
 90 95 100
 Cys Phe Asn Thr Xaa Leu Leu Xaa Ile Xaa Gly Phe Leu Tyr Ser Glu
 105 110 115
 Xaa Ser Ala Pro Xaa Phe Ala Ile Phe Asn Phe Val Gln Ser Ile Cys
 120 125 130
 Ala Ala Val Ala Phe Phe Tyr Ser Asn Tyr Leu Leu Leu His Trp Gln
 135 140 145
 Leu Leu Val Met Val Ile Phe Gly Phe Xaa Gly Thr Ile Ser Phe Phe
 150 155 160 165
 Thr Val Glu Trp Glu Xaa Ala Ala Phe Val Xaa Arg Gly Ser Asp Tyr
 170 175 180

Arg Ser Ile

<210> 404
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -80...-1

<400> 404
 Met Ser Thr Trp Tyr Leu Ala Leu Asn Lys Ser Tyr Lys Asn Lys Asp
 -80 -75 -70 -65
 Ser Val Arg Ile Tyr Leu Ser Leu Cys Thr Val Ser Ile Lys Phe Thr
 -60 -55 -50
 Tyr Phe His Asp Ile Gln Thr Asn Cys Leu Thr Thr Trp Lys His Ser
 -45 -40 -35
 Arg Cys Arg Phe Tyr Trp Ala Phe Gly Gly Ser Ile Leu Gln His Ser
 -30 -25 -20
 Val Asp Pro Leu Val Leu Phe Leu Ser Leu Ala Leu Leu Val Thr Pro
 -15 -10 -5
 Thr Ser Thr Pro Ser Ala Lys Ile Gln Ser Leu Gln Ile Asp Leu Pro
 1 5 10 15
 Gly Gly Trp Arg Leu Ala Thr Asp Arg Ile Phe Thr Leu Ser Pro Val
 20 25 30
 Pro Met Asp Xaa Pro Leu Ile Leu His Gln Leu
 35 40

<210> 405
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 405
 Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp Leu Ile
 -25 -20 -15
 Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu Leu Pro
 -10 -5 1 5
 Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu Leu Leu
 10 15 20
 Ile Phe Ile Ser Ile Xaa Gly Ile Leu Tyr Lys Phe Xaa Asp Val Leu
 25 30 35
 Leu Tyr Phe Pro Xaa Gln Xaa Ser Ser Ser Arg Leu Tyr Asp Ser His
 40 45 50
 Ala His Trp Xaa Ser Xaa
 55 60

<210> 406
 <211> 162
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -31...-1

<400> 406

Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu Ala Val Thr
 -30 -25 -20
 Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro
 -15 -10 -5 1
 Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys
 5 10 15
 Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn
 20 25 30
 Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val
 35 40 45
 Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn
 50 55 60 65
 Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser
 70 75 80
 Cys Arg Asn Val Asn Gly Tyr Ser Tyr Asn Glu Gln Ser His Val Ser
 85 90 95
 Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp Ile Pro Cys
 100 105 110
 Phe Gly Phe Val Lys Xaa Xaa His Cys Arg Val Xaa Trp Asn Trp Glu
 115 120 125
 Pro Asn
 130

<210> 407

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37...-1

<400> 407

Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile
 -35 -30 -25
 Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe
 -20 -15 -10
 Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu
 -5 1 5 10
 Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Xaa Gln
 15 20 25
 Xaa Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly
 30 35 40
 Gly Phe Ser Phe Cys Gln Xaa Arg Leu Asn Lys Arg Lys Glu Tyr Met
 45 50 55
 Val Arg
 60

<210> 408

<211> 70

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15...-1

<400> 408

Met Arg Phe Leu Pro Cys Cys Leu Leu Trp Ser Val Phe Asn Pro Glu
-15 -10 -5 1
Ser Leu Asn Cys His Tyr Phe Xaa Xaa Glu Xaa Cys Ile Phe Xaa Ser
5 10 15
Leu Gln Tyr Tyr Glu Ile Ser Leu Gln Glu Lys Leu Leu Gly Phe Leu
20 25 30
Trp Leu Cys Phe Leu Ser Tyr Phe Phe Arg Ala Val Tyr Phe Leu Ile
35 40 45
Asp Phe Ser Ser Phe Thr
50 55

<210> 409

<211> 60

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -45...-1

<400> 409

Met His Ser Leu Phe Ile Ala Ser Leu Lys Val Leu Phe Tyr Tyr Ser
-45 -40 -35 -30
Phe Ser Phe Arg Phe Asn Trp Phe Asp Cys Leu Leu His Asn Leu Gly
-25 -20 -15
Glu Asn Phe Leu Ser Leu Leu Ser Lys Ser Cys Ser Ala Asp Pro Ser
-10 -5 1
Gly Ser Thr Phe Met Arg Asp Ile Glu Thr Asn Lys
5 10 15

<210> 410

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -22...-1

<400> 410

Met Pro Glu Ala Val Glu Gln Ser Ala His Leu Phe Val Thr Trp Ser
-20 -15 -10
Ser Gln Arg Ala Leu Ser His Pro Ala Pro Phe Leu Thr Xaa Xaa Lys
-5 1 5 10
Asn Pro Phe Leu Trp Lys Leu
15

<210> 411

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23...-1

<400> 411

```

Met Ala Phe Gln Ser Leu Leu Glu Met Lys Phe Phe Leu Cys Ala Ala
      -20                      -15                      -10
Phe Pro Leu Gly Ala Gly Val Lys Met Phe His Tyr Leu Gly Pro Gly
      -5                      1                      5
Lys Pro Leu Xaa Gln Ala Ser Pro Ser Pro His Pro His Arg Xaa Arg
10                      15                      20                      25
Ile Trp Pro

```

<210> 412

<211> 95

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48...-1

<400> 412

```

Met Ala Ser Ser His Trp Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr
      -45                      -40                      -35
Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro Phe His Asp Asn Trp Asn
      -30                      -25                      -20
Thr Ala Cys Phe Val Ile Leu Leu Leu Phe Ile Phe Thr Val Val Ser
      -15                      -10                      -5
Leu Val Val Leu Ala Phe Leu Tyr Glu Val Leu Xaa Xaa Cys Cys Cys
1                      5                      10                      15
Val Lys Asn Lys Thr Val Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu
      20                      25                      30
Xaa Xaa Met Met Asp Asn Ile Arg Lys Arg Glu Thr Glu Val Val
      35                      40                      45

```

<210> 413

<211> 60

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -32...-1

<400> 413

```

Met Asp Glu Tyr Ser Trp Trp Cys His Val Leu Glu Val Val Lys Gly
      -30                      -25                      -20
Gln Met Phe Thr Phe Ile Asn Ile Thr Leu Trp Leu Gly Ser Leu Cys
      -15                      -10                      -5
Gln Arg Phe Phe Tyr Ala Ser Gly Thr Tyr Phe Leu Ile Tyr Ile Ser
1                      5                      10                      15
Thr Val Thr Pro Ser Trp Arg Leu Cys Leu Val Ser
      20                      25

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```

<400> 415
Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe
      -80                      -75                      -70
His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly
      -65                      -60                      -55
Val Ser Leu Pro Gly Ile Leu Ala Ala Lys Cys Gly Ala Glu Val Ile
-50                      -45                      -40                      -35
Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln,
                      -30                      -25                      -20
Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu Thr
                      -15                      -10                      -5
Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp Ile
      1                      5                      10
Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Xaa Phe Glu Asp Ile
15                      20                      25                      30
Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln Leu
      35                      40                      45

```


Trp Ser Thr Tyr Gln Val Arg Xaa Ala Asp Trp Ser Leu Glu Ala Leu
 50 55 60
 Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser Phe
 65 70 75
 Asp Ala Asp Lys Glu Xaa Ile Ala Glu Ser Thr Leu Pro Gly Arg His
 80 85 90
 Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu
 95 100 105

<210> 416
 <211> 114
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

<400> 416
 Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro Trp Asn Arg Val Arg
 -60 -55 -50 -45
 Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr Val Gln Asn Pro Gly
 -40 -35 -30
 Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile Lys Glu Cys His Leu
 -25 -20 -15
 Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp Ala Glu Thr Asp Val
 -10 -5 1
 Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg Met Gly Arg His Lys
 5 10 15 20
 Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys Leu Lys Arg Leu Lys
 25 30 35
 Asn Met Asn Leu Glu Gly Ser Ile Gln Asp Leu Phe Glu Leu Phe Ser
 40 45 50
 Ser Lys

<210> 417
 <211> 161
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -108...-1

<400> 417
 Met Thr Ser Gly Gln Ala Arg Ala Ser Xaa Gln Ser Pro Gln Ala Leu
 -105 -100 -95
 Glu Asp Ser Gly Pro Val Asn Ile Ser Val Ser Ile Thr Leu Thr Leu
 -90 -85 -80
 Asp Pro Leu Lys Pro Phe Gly Gly Tyr Ser Arg Asn Val Thr His Leu
 -75 -70 -65
 Tyr Ser Thr Ile Leu Gly His Gln Ile Gly Leu Ser Gly Arg Glu Ala
 -60 -55 -50 -45
 His Glu Glu Ile Asn Ile Thr Phe Thr Leu Pro Thr Ala Trp Ser Ser
 -40 -35 -30
 Asp Asp Cys Ala Leu His Gly His Cys Glu Gln Val Val Phe Thr Ala
 -25 -20 -15
 Cys Met Thr Leu Thr Ala Ser Pro Gly Val Phe Pro Ser Leu Tyr Ser

```

      -10      -5      1
His Arg Thr Val Phe Leu Thr Arg Thr Ala Thr Pro Arg Ser Gly Thr
5          10          15          20
Arg Ser Ser Gln Leu Pro Glu Met Pro Thr Gln Asn Thr Pro Lys Ile
      25          30          35
Thr Ile Leu Ser Gly Val Ile Arg Gly Pro Leu Glu Lys Ser Ile Met
      40          45          50
Leu

```

<210> 418
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

```

<400> 418
Met Leu Gly Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
-20          -15          -10
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
-5          1          5          10
Met Glu Arg Arg Val Lys Asn Asp Leu Met Ser Phe Leu Ser Thr Val
      15          20          25
Leu Leu Ser Phe His Ser Ser Asn Ala Arg Val Ser His Cys Glu Pro
      30          35          40
Leu Arg Met
      45

```

<210> 419
 <211> 332
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

```

<400> 419
Met Ile Xaa Leu Arg Asp Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp
-30          -25          -20
Thr Arg Gln Leu Pro Leu Leu Thr Ser Ala Leu His Gly Leu Gln Gln
-15          -10          -5
Gln His Pro Ala Phe Ser Gly Val Ala Arg Leu Ala Lys Arg Trp Val
1          5          10          15
Arg Ala Gln Leu Leu Gly Glu Gly Phe Ala Asp Glu Ser Leu Asp Leu
      20          25          30
Val Ala Ala Ala Leu Phe Leu His Pro Glu Pro Phe Thr Pro Pro Ser
      35          40          45
Ser Pro Gln Val Gly Phe Leu Arg Phe Leu Phe Leu Val Ser Thr Phe
      50          55          60
Asp Trp Lys Asn Asn Pro Leu Phe Val Asn Leu Asn Asn Glu Leu Thr
65          70          75          80
Val Glu Glu Gln Val Glu Ile Arg Ser Gly Phe Leu Ala Ala Arg Ala
      85          90          95
Gln Leu Pro Val Met Val Ile Val Thr Pro Gln Xaa Arg Lys Asn Ser
      100          105          110

```

```

Val Trp Thr Gln Asp Gly Pro Ser Ala Gln Ile Leu Gln Gln Leu Val
    115                      120                      125
Val Leu Ala Ala Glu Xaa Leu Pro Met Leu Xaa Xaa Gln Leu Met Asp
    130                      135                      140
Pro Arg Gly Pro Gly Asp Ile Arg Thr Xaa Phe Arg Pro Pro Leu Asp
    145                      150                      155                      160
Ile Tyr Asp Val Leu Ile Arg Leu Ser Pro Arg His Ile Pro Arg His
    165                      170                      175
Arg Gln Ala Val Asp Ser Pro Ala Ala Ser Phe Cys Arg Gly Leu Leu
    180                      185                      190
Ser Gln Pro Gly Pro Ser Ser Leu Met Pro Val Leu Gly Xaa Asp Pro
    195                      200                      205
Pro Gln Leu Tyr Leu Thr Gln Leu Xaa Glu Ala Phe Gly Asp Leu Ala
    210                      215                      220
Leu Phe Phe Tyr Asp Gln His Gly Gly Glu Val Ile Gly Val Leu Trp
    225                      230                      235                      240
Lys Pro Thr Ser Phe Gln Pro Gln Pro Phe Lys Ala Ser Ser Thr Lys
    245                      250                      255
Gly Arg Met Val Met Ser Arg Gly Gly Glu Leu Val Met Val Pro Asn
    260                      265                      270
Val Glu Ala Ile Leu Glu Asp Phe Ala Val Leu Gly Glu Gly Leu Val
    275                      280                      285
Gln Thr Val Glu Ala Arg Ser Glu Arg Trp Thr Val
    290                      295                      300

```

<210> 420
 <211> 65
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

```

<400> 420
Met Gly Gly Ile Trp Asn Ala Leu Ser Met Ser Ser Phe Ser Phe His
    -15                      -10                      -5
Ser Ser Ser Cys Ser Ala Leu Ser Ala Lys Ser Leu Leu Ser Arg His
    1                      5                      10
His Ile Leu Gln Gln Phe Leu Val Arg Lys Ser Val Pro Leu Glu Asn
    15                      20                      25
Ala Ser Leu Pro Phe Pro His Leu Gly Ser Ser Leu Phe Lys Ile Val
    30                      35                      40                      45
Gly

```

<210> 421
 <211> 57
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

```

<400> 421
Met Pro Thr Gly Lys Gln Leu Ala Asp Ile Gly Tyr Lys Thr Phe Ser
    -30                      -25                      -20                      -15
Thr Ser Met Met Leu Leu Thr Val Tyr Gly Gly Tyr Leu Cys Ser Val

```

```
<210> 424
<211> 69
<212> PRT
<213> Homo sapiens
```

<220>

<221> SIGNAL

<222> -29...-1

<400> 424

```

Met Thr Cys Arg Gly Ser Cys Ser Tyr Ala Thr Arg Arg Ser Pro Ser
      -25      -20      -15
Glu Leu Ser Leu Leu Pro Ser Ser Leu Trp Val Leu Ala Thr Ser Ser
      -10      -5      1
Pro Thr Ile Thr Ile Ala Leu Ala Met Ala Ala Gly Asn Leu Cys Pro
      5      10      15
Leu Pro Ser Ser Xaa Arg Xaa Lys Arg Arg Trp Cys Gln Ala Xaa Gln
20      25      30      35
Gln Xaa Ala Leu Leu
      40

```

<210> 425

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -56...-1

<400> 425

```

Met Val Pro Trp Pro Arg Gly Lys Val Lys Thr Ala Pro Ile Pro Ile
      -55      -50      -45
Ser Arg Phe Pro Phe Leu Pro Thr His Asp Pro Pro Thr Pro Ala His
-40      -35      -30      -25
Trp Ser Pro Ala Ser His Gln Gln Phe Lys His Xaa Ser Pro Leu Leu
      -20      -15      -10
Thr Leu Ala Leu Leu Gly Gln Cys Ser Leu Phe Xaa Asn Leu Arg Lys
      -5      1      5
Lys Leu Ala Gly Gln Lys Ala Lys Lys Leu Pro Ser Phe Ser Ser Leu
      10      15      20
Pro Leu Thr Leu Trp Pro Leu Thr Pro Gln Phe Ala Glu Leu Thr Thr
25      30      35      40
Val Ala Gln Lys Lys Leu Arg Trp Ser Gly Thr Leu Gly Trp Gly Pro
      45      50      55
Val Pro Ser Trp Val Gln Phe Phe Leu Gly
      60      65

```

<210> 426

<211> 41

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -30...-1

<400> 426

```

Met Ala Cys Glu Thr His Gly Val Leu Val Pro Ala His Leu Ser Gly
-30      -25      -20      -15
Leu Ile Thr Cys Leu Leu Ala Phe Trp Val Pro Ala Ser Cys Ile Gln
      -10      -5      1

```

Arg Cys Ser Gly Ser Pro Leu Pro Leu
 5 10

<210> 427
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 427
 Met Ala Pro His Thr Ala Ser Phe Gly Val Cys Pro Leu Leu Ser Val
 -35 -30 -25
 Thr Arg Val Val Ala Thr Glu His Trp Leu Phe Leu Ala Ser Leu Ser
 -20 -15 -10 -5
 Gly Ile Lys Thr Tyr Gln Ser Tyr Ile Ser Val Phe Cys Lys Val Thr
 1 5 10
 Leu Ile

<210> 428
 <211> 136
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 428
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala
 -15 -10 -5
 Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu
 1 5 10
 Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg
 15 20 25 30
 Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu Ala Thr Leu
 35 40 45
 Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp
 50 55 60
 Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His Arg Glu Thr Gly
 65 70 75
 Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg Arg Asn Pro Arg
 80 85 90
 Gln Leu Ser Pro Ser Trp Ala Xaa Arg Lys Ile Arg Xaa Glu Asn Xaa
 95 100 105 110
 Met Pro Gly Leu Ser Gly Val Leu
 115

<210> 429
 <211> 194
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -65...-1

<400> 429

Met Gln Asp Ala Pro Leu Ser Cys Leu Ser Pro Thr Lys Trp Ser Ser
 -65 -60 -55 -50
 Val Ser Ser Ala Asp Ser Thr Glu Lys Ser Ala Ser Ala Ala Gly Thr
 -45 -40 -35
 Arg Asn Leu Pro Phe Gln Phe Cys Leu Arg Gln Ala Leu Arg Met Lys
 -30 -25 -20
 Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr Gly Val Glu
 -15 -10 -5
 Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile Phe Ser Arg Ala
 1 5 10 15
 Gly Leu Asp Asn Xaa Arg Gly Phe Ser Leu Gly Asn Trp Ile Cys Met
 20 25 30
 Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr Ala Gln Thr Val Leu Asp
 35 40 45
 Asp Gly Ser Ile Asp Tyr Gly Ile Phe Gln Ile Asn Ser Phe Ala Trp
 50 55 60
 Cys Arg Arg Gly Lys Leu Lys Glu Asn Asn His Cys His Val Ala Cys
 65 70 75
 Ser Ala Leu Xaa Thr Asp Asp Leu Thr Asp Ala Ile Ile Cys Ala Xaa
 80 85 90 95
 Lys Ile Val Lys Glu Thr Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys
 100 105 110
 Lys His Cys Glu Gly Arg Asp Leu Ser Xaa Trp Lys Lys Gly Cys Glu
 115 120 125
 Val Ser

<210> 430

<211> 141

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -69...-1

<400> 430

Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
 -65 -60 -55
 Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln
 -50 -45 -40
 Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile Lys Val Ile
 -35 -30 -25
 Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile
 -20 -15 -10
 Ile Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser
 -5 1 5 10
 Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Val Xaa
 15 20 25
 Lys Xaa Ser Glu Glu Gly Arg Met Gly Gln Xaa Gly Glu Glu Xaa Xaa
 30 35 40
 Asn Ser Leu Asn Phe Pro Xaa Ala Ser Leu Leu Xaa Leu Ile Cys Gln
 45 50 55
 Xaa Gln Gly Phe Asn Gly Glu Ser Cys Ser Pro Val Gly
 60 65 70

```

<400> 432
Met Gln Val Pro His Leu Arg Val Trp Thr Gln Val Xaa Asp Thr Phe
  -35                -30                -25
Ile Gly Tyr Arg Asn Leu Gly Phe Thr Ser Met Cys Ile Leu Phe His
-20                -15                -10                -5
Cys Leu Leu Ser Phe Gln Val Phe Lys Lys Lys Arg Lys Leu Xaa Leu
      1                5                10

```



```
<210> 435
<211> 121
```

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 435
 Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
 -15 -10 -5
 Ser Ala Gly Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln
 1 5 10 15
 Cys Phe Lys Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser
 20 25 30
 Pro Leu Asp Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Ser
 35 40 45
 Glu Ser Pro Pro Gly Arg Gly Xaa Val Pro Xaa Ala Gly Glu Xaa Pro
 50 55 60
 Val Pro Pro Pro Leu Xaa Asp Leu Xaa Met Thr Pro Arg Xaa Xaa Arg
 65 70 75 80
 Ala Trp Gly Pro Val Gly Pro Lys Val Pro Pro Ala Val Ser Pro Ala
 85 90 95
 Leu Gly Ser Gly Glu His Pro Xaa Xaa
 100 105

<210> 436
 <211> 162
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 436
 Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
 -15 -10 -5
 Ser Ala Gly Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln
 1 5 10 15
 Cys Phe Lys Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser
 20 25 30
 Pro Leu Asp Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys
 35 40 45
 Trp Ser Val Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro
 50 55 60
 Asn Asp Asn Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly
 65 70 75 80
 Val Ile Thr Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu
 85 90 95
 Thr Pro Gln Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln
 100 105 110
 Asp Pro Ser Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu
 115 120 125
 Pro Leu Cys Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln
 130 135 140
 Glu Gly
 145

<210> 437
 <211> 110
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 437
 Met Xaa Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu Leu
 -20 -15 -10 -5
 Gly Xaa Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg Lys Ile
 1 5 10
 Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val Ala Asp Leu
 15 20 25
 Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp Asp Gly Lys Gly
 30 35 40
 Cys Glu Met Ile Cys Tyr Cys Asn Phe Lys Arg Ile Ala Leu Leu Pro
 45 50 55 60
 Lys Arg Arg Phe Leu Trp Thr Lys Asp Leu Phe Arg Asp Ser Leu Gln
 65 70 75
 Gln Ser Met Arg Ile Phe Met Tyr Ser Gly Glu His His Ser
 80 85 90

<210> 438
 <211> 71
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 438
 Met Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val
 -15 -10 -5 1
 Gly Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile
 5 10 15
 Cys Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys
 20 25 30
 Val Glu Trp Ser Ala Phe Leu Glu Ala Xaa Asp Asn Leu Arg Leu Ile
 35 40 45
 Gln Val Pro Arg Arg Ala Gly
 50 55

<210> 439
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 439
 Met Lys Ser Ala Lys Leu Gly Phe Leu Leu Arg Phe Phe Ile Phe Cys
 -20 -15 -10

Ser Leu Asn Thr Leu Leu Leu Gly Gly Val Asn Lys Ile Ala Glu Lys
 -5 1 5
 Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys Leu Asp Met Asn Phe Gly
 10 15 20
 Ser Cys Tyr Glu Val His Phe Arg Tyr Phe Tyr Asn Arg Thr Ser Lys
 25 30 35 40
 Arg Cys Glu Thr Phe Val Phe Ser Ser Cys Asn Gly Asn Leu Asn Asn
 45 50 55
 Phe Lys Leu Lys Ile Glu Arg Glu Val Xaa Cys Val Ala Lys Tyr Lys
 60 65 70
 Pro Pro Arg
 75

<210> 440
 <211> 169
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 440
 Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser Leu Leu Lys Val Leu
 -25 -20 -15 -10
 Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp Ser Thr Gln Ala Ser
 -5 1 5
 Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr Gln Arg Phe Phe Ala
 10 15 20
 Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr Cys Arg Leu Arg Ala
 25 30 35
 Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln Leu Asp Gln Tyr Glu
 40 45 50 55
 Asn His Gly Leu Val Pro Asp Gly Ala Val Cys Ser Asn Leu Pro Tyr
 60 65 70
 Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr His Tyr Arg Cys Ser
 75 80 85
 Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys Ser Gln Pro Val Ser
 90 95 100
 Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu Xaa Ser Ala Glu Val
 105 110 115
 Ser Pro Thr Thr Asp Asp Leu Pro His Leu Thr Pro Leu His Ser Asp
 120 125 130 135
 Arg Thr Pro Asp Leu Pro Ala Leu Ala
 140

<210> 441
 <211> 167
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -76...-1

<400> 441
 Met Gly Asp Tyr Leu Leu Arg Gly Tyr Arg Met Leu Gly Glu Thr Cys
 -75 -70 -65

Ala Asp Cys Gly Thr Ile Leu Leu Gln Asp Lys Gln Arg Lys Ile Tyr
 -60 -55 -50 -45
 Cys Val Ala Cys Gln Glu Leu Asp Ser Asp Val Asp Lys Asp Asn Pro
 -40 -35 -30
 Ala Leu Asn Ala Gln Ala Ala Leu Ser Gln Ala Arg Glu His Gln Leu
 -25 -20 -15
 Ala Ser Ala Ser Glu Leu Pro Leu Gly Ser Arg Pro Ala Pro Gln Pro
 -10 -5 1
 Pro Val Pro Arg Pro Glu His Cys Glu Gly Ala Ala Ala Gly Leu Lys
 5 10 15 20
 Ala Ala Gln Gly Pro Pro Ala Pro Ala Val Pro Pro Asn Thr Xaa Val
 25 30 35
 Met Ala Cys Thr Gln Thr Ala Leu Leu Gln Lys Leu Thr Trp Ala Ser
 40 45 50
 Ala Glu Leu Gly Ser Xaa Thr Ser Xaa Gly Lys Xaa Ala Ser Ser Cys
 55 60 65
 Val Ala Leu Ser Ala His Val Arg Arg Pro Cys Ala Ala Cys Ser Ser
 70 75 80
 Tyr Ser Thr Lys Arg Ser Pro
 85 90

<210> 442
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 442
 Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg
 -15 -10 -5 1
 Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg
 5 10 15
 Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys Xaa Arg Thr Lys Tyr Glu
 20 25 30
 Thr Pro Arg Lys Xaa Xaa Gly Lys Lys Gly Gly Asn Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Leu Ser Lys Arg Asp
 50 55

<210> 443
 <211> 381
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 443
 Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser
 -30 -25 -20
 Val Gly Ala Asn Xaa Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln
 -15 -10 -5
 Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser
 1 5 10 15

```

<400> 444
Met Tyr Tyr Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His
              -10                      -5                      1
Leu Pro Ile Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Leu Thr
              5                      10                      15
Val Tyr Pro Thr Ser Ala Gly
      20                      25

```

<210> 445
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 445
 Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
 -35 -30 -25
 Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
 -20 -15 -10
 Ser Pro Cys Leu Thr Ala Pro Lys Ser Pro Arg Leu Ala Met Met Pro
 1 5 10
 Asp Asn

<210> 446
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 446
 Met Thr Pro Trp Cys Leu Ala Cys Leu Gly Arg Arg Pro Leu Ala Ser
 -25 -20 -15
 Leu Gln Trp Ser Leu Thr Leu Ala Trp Cys Gly Ser Gly Ser His Trp
 -10 -5 1 5
 Thr Glu Arg Pro Xaa Gln Xaa Ser Pro Trp Xaa Ser Leu Ser Ala Thr
 10 15 20
 Thr Arg Gly
 25

<210> 447
 <211> 242
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 447
 Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
 -30 -25 -20 -15
 Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
 -10 -5 1
 Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
 5 10 15
 Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
 20 25 30
 Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly

```

35          40          45          50
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
                    55          60          65
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
                    70          75          80
Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
                    85          90          95
Pro Xaa Glu Gly Xaa Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
                    100          105          110
Glu Lys Glu Ala Leu Val Pro Xaa Gln Lys Ala Thr Asp Ser Phe His
115          120          125          130
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
                    135          140          145
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Xaa Glu
                    150          155          160
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
                    165          170          175
His Lys Asp Xaa Leu Xaa Xaa Gly Thr Glu Ser Ser Ser His Ser Arg
180          185          190
Leu Ser Pro Arg Lys Xaa His Leu Leu Tyr Ile Leu Xaa Pro Ser Arg
195          200          205          210
Gln Leu

```

<210> 448
 <211> 154
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

```

<400> 448
Met Gly Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu
-60          -55          -50          -45
Arg Gln Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys
          -40          -35          -30
Arg Val Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu
          -25          -20          -15
Val Arg Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln
          -10          -5          1
Cys Trp Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln
5          10          15          20
Ala Leu Leu Gly Val Tyr Val Ile Gln Glu Gln Ala Ala Val Lys Leu
          25          30          35
Gln Ser Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met
          40          45          50
Cys Asn Ala Leu Cys Leu Phe Gln Val Pro Lys Ser Ser Leu Ala Phe
          55          60          65
Gln Thr Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln
70          75          80
Pro Glu Phe His Ile Glu Ile Leu Ser Ile
85          90

```

<210> 449
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -61...-1

<400> 449

Met Asn Ala Ala Ile Asn Thr Gly Pro Ala Pro Ala Val Thr Lys Thr
 -60 -55 -50
 Glu Thr Glu Val Gln Asn Pro Asp Val Leu Trp Asp Leu Asp Ile Pro
 -45 -40 -35 -30
 Glu Ala Arg Ser His Ala Asp Gln Asp Ser Asn Pro Lys Ala Glu Ala
 -25 -20 -15
 Leu Leu Pro Cys Asn Leu His Cys Ser Trp Leu His Ser Ser Pro Arg
 -10 -5 1
 Pro Asp Pro His Ser His Phe Pro Ser Xaa Arg Arg Cys Pro Leu Pro
 5 10 15
 His Pro Cys Ala Thr Tyr Pro Pro Xaa
 20 25

<210> 450

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 450

Met Arg Met Ser Leu Ala Gln Arg Val Leu Leu Thr Trp Leu Phe Thr
 -25 -20 -15
 Leu Leu Phe Leu Ile Met Leu Val Leu Lys Leu Asp Glu Lys Ala Pro
 -10 -5 1 5
 Trp Asn Trp Phe Leu Ile Phe Ile Pro Val Trp Ile Phe Asp Thr Ile
 10 15 20
 Leu Leu Val Leu Leu Ile Val Lys Met Ala Gly Arg Cys Lys Ser Gly
 25 30 35
 Phe Asp Leu Asp Met Asp His Thr Ile
 40 45

<210> 451

<211> 54

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -34...-1

<400> 451

Met Ile Pro Leu Ile Ser His Leu Ala Glu Ala Ala Pro Pro Thr Ser
 -30 -25 -20
 Trp Ser Leu Ile Ser Ser Val Leu Asn Val Gly His Leu Leu Phe Ser
 -15 -10 -5
 Ser Ala Cys Ser Val Ser Leu Glu Ala Leu Ser Thr Arg Asn Ile Lys
 1 5 10
 Ala Ile Ile Leu Met Lys
 15 20

<210> 452
 <211> 121
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38...-1

<400> 452
 Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn Ser Val Ala
 -35 -30 -25
 Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu Ser Cys Leu
 -20 -15 -10
 Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala Gly Thr Arg
 -5 1 5 10
 Phe Lys Thr Ala Phe Gln Leu Leu Asp Phe Ile Leu Ala Val Leu Trp
 15 20 25
 Ala Val Val Trp Phe Met Gly Phe Cys Phe Leu Ala Asn Gln Trp Gln
 30 35 40
 His Ser Pro Pro Lys Glu Xaa Leu Leu Gly Ser Ser Ser Ala Gln Ala
 45 50 55
 Ala Ile Gly Xaa His Leu Leu Leu His Pro Cys Leu Asp Ile Pro Xaa
 60 65 70
 Leu Pro Gly Xaa Pro Gly Pro Pro Lys
 75 80

<210> 453
 <211> 166
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 453
 Met Ser Thr Val Gly Leu Phe His Phe Pro Thr Pro Leu Thr Arg Ile
 -35 -30 -25
 Cys Pro Ala Pro Trp Gly Leu Arg Leu Trp Glu Lys Leu Thr Leu Leu
 -20 -15 -10
 Ser Pro Gly Ile Ala Val Thr Pro Val Gln Met Ala Gly Lys Lys Asp
 -5 1 5 10
 Tyr Pro Ala Leu Leu Ser Leu Asp Glu Asn Glu Leu Glu Glu Gln Phe
 15 20 25
 Val Lys Gly His Gly Pro Gly Gly Gln Ala Thr Asn Lys Thr Ser Asn
 30 35 40
 Cys Val Val Leu Lys Xaa Ile Pro Ser Gly Ile Val Val Lys Cys His
 45 50 55
 Gln Thr Arg Ser Val Asp Gln Asn Arg Lys Leu Ala Arg Lys Ile Leu
 60 65 70 75
 Gln Glu Lys Val Xaa Val Phe Tyr Asn Gly Glu Asn Ser Pro Val His
 80 85 90
 Lys Glu Lys Arg Glu Ala Ala Lys Lys Lys Gln Glu Arg Lys Lys Arg
 95 100 105
 Ala Lys Glu Thr Leu Glu Lys Lys Xaa Leu Leu Lys Xaa Leu Trp Glu
 110 115 120

Ser Ser Lys Lys Val His
125

<210> 454
<211> 180
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26...-1

<400> 454
Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
-25 -20 -15
Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
-10 -5 1 5
Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
10 15 20
Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
25 30 35
Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
40 45 50
Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
55 60 65 70
Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
75 80 85
Val Xaa Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
90 95 100
Gly Lys Met Ser Xaa Tyr Leu Asp Xaa Leu Lys Val Gly Asp Xaa Val
105 110 115
Glu Phe Xaa Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
120 125 130
Phe Asn Ile Gln Pro Asn Lys Asn Leu His Gln Asn Pro Glu Trp Arg
135 140 145 150
Arg Asn Trp Glu

<210> 455
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -64...-1

<400> 455
Met Thr Pro Arg Ile Leu Ser Glu Val Gln Phe Ser Ala Phe Cys Pro
-60 -55 -50
Tyr Trp Thr Ile Ala Arg Ile Leu Glu Arg Val Gly Ser Ala Cys Phe
-45 -40 -35
Arg Leu Glu Leu Cys Ala Ala Ile Val Gly Tyr Phe Val Leu Asp Val
-30 -25 -20
Arg Thr Phe Leu Phe Ile Val Val Cys Val Ile Cys Val Thr Leu Asn
-15 -10 -5
Phe Pro Arg Phe Tyr Phe Leu Cys Leu Ser Ser Leu Thr Ala Phe Gly
1 5 10 15
Thr Pro Pro Ile Gly Val His Ile Pro Ser Pro

20

25

<210> 456
 <211> 257
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 456
 Met Arg Arg Ile Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa
 -20 -15 -10
 Leu Leu Leu Leu Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser
 -5 1 5
 Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro
 10 15 20 25
 Trp Cys Glu Ala His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr
 30 35 40
 Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys
 45 50 55
 Val Tyr Ala Thr Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu
 60 65 70
 Val Gly Arg Asp Leu Arg Met Leu Leu Cys Asp Ile Lys Pro Gln Ile
 75 80 85
 Lys Thr Ser Asp Pro Ser Thr Leu Gln Val Xaa Xaa Phe Cys Gln Arg
 90 95 100 105
 Glu Ala Glu Arg Cys Thr Gly Ala Ser Trp Gln Phe Ala Thr Asn Gly
 110 115 120
 Glu Lys Ser Leu Leu Phe Asp Ala Met Asn Met Thr Trp Thr Val Ile
 125 130 135
 Asn His Glu Ala Ser Xaa Ile Lys Glu Thr Trp Lys Lys Asp Arg Xaa
 140 145 150
 Leu Glu Xaa Tyr Phe Arg Lys Leu Ser Lys Gly Asp Cys Asp His Trp
 155 160 165
 Leu Arg Glu Phe Leu Gly His Trp Glu Ala Met Pro Xaa Pro Xaa Val
 170 175 180 185
 Ser Pro Xaa Asn Ala Ser Xaa Ile His Trp Ser Ser Ser Xaa Leu Pro
 190 195 200
 Xaa Xaa Trp Ile Ile Leu Gly Ala Phe Ile Leu Leu Xaa Leu Met Gly
 205 210 215
 Ile Val Leu Ile Cys Val Trp Trp Gln Asn Gly Xaa Xaa Ser Thr Xaa
 220 225 230
 Xaa

<210> 457
 <211> 193
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

<400> 457
 Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu Pro
 -60 -55 -50 -45

[illegible]

```
<210> 458
<211> 107
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -28..-1
```

<400> 458															
Met	Val	Leu	Thr	Leu	Gly	Glu	Ser	Trp	Pro	Val	Leu	Val	Gly	Arg	Arg
			-25					-20					-15		
Phe	Leu	Ser	Leu	Ser	Ala	Ala	Asp	Gly	Ser	Asp	Gly	Ser	His	Asp	Ser
		-10					-5					1			
Trp	Asp	Val	Glu	Arg	Val	Ala	Glu	Trp	Pro	Trp	Leu	Ser	Gly	Thr	Ile
5					10					15					20
Arg	Ala	Val	Ser	His	Thr	Asp	Val	Thr	Lys	Lys	Asp	Leu	Lys	Val	Cys
				25					30					35	
Val	Glu	Phe	Xaa	Gly	Glu	Ser	Trp	Arg	Lys	Arg	Arg	Trp	Ile	Glu	Val
			40					45					50		
Tyr	Ser	Leu	Leu	Arg	Lys	Ala	Phe	Leu	Val	Lys	His	Asn	Leu	Val	Leu
		55					60					65			
Ala	Glu	Arg	Lys	Ser	Pro	Glu	Ile	Ser	Trp	Gly					
		70				75									

```
<210> 459
<211> 121
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -13...-1
```

<400> 459

```

Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr
      -10                -5                1
Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr
      5                10                15
Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys
20                25                30                35
Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn Ala Gln Leu Arg Thr
      40                45                50
Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val Xaa Phe Gly Gly Arg
      55                60                65
Met Xaa Thr Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg
      70                75                80
Thr Glu Phe Gln Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln
      85                90                95
Phe Leu Ile Pro Asn Leu Ala Leu Asn
100                105

```

<210> 460

<211> 44

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17...-1

<400> 460

```

Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp
      -15                -10                -5
Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys Tyr Val Ser Tyr Leu
      1                5                10                15
Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg Ile
      20                25

```

<210> 461

<211> 109

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -13...-1

<400> 461

```

Met Cys Leu Leu Thr Ala Leu Val Thr Gln Val Ile Ser Leu Arg Lys
      -10                -5                1
Asn Ala Glu Arg Thr Cys Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro
      5                10                15
Ser Pro Arg Ile Tyr Cys Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro
20                25                30                35
Thr Val Tyr Ser Ser Ala Pro Phe His Ala Pro Leu Pro Val Gln Asn
      40                45                50
Ser Leu Trp Gly His Pro Leu His Gly Cys Ser Trp Gln Cys His His
      55                60                65
Pro Gln Gly Gln Asn Leu Gln Pro Ala Ser Leu Xaa Thr His Leu Ser
      70                75                80
Lys Pro Lys Arg His Phe Xaa Lys Lys Xaa Cys Gln Ala

```

85

90

95

<210> 462
 <211> 143
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 462
 Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val Glu Met Val Gln Ala
 -40 -35 -30
 Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu Glu Gly Ile Leu Ile
 -25 -20 -15 -10
 Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr Tyr Lys Leu Gln Glu
 -5 1 5
 Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu Leu Ile Glu Glu Trp
 10 15 20
 Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys Asp His Pro Ala Leu
 25 30 35
 Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His Lys Thr Val Val Asn
 40 45 50 55
 Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn Phe Leu Gly Leu Leu
 60 65 70
 Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala Ser Leu Lys Lys Tyr
 75 80 85
 Gly Val Gly Thr Cys Gly Pro Cys Gly Phe Tyr Gly Thr Phe Glu
 90 95 100

<210> 463
 <211> 232
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 463
 Met Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val
 -30 -25 -20 -15
 Ser Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Xaa
 -10 -5 1
 Xaa Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu
 5 10 15
 Val Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu
 20 25 30
 Thr Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu
 35 40 45 50
 Thr Leu Arg Ile Asp Val Leu Xaa Pro Glu Xaa Leu Lys Ser Glu Ser
 55 60 65
 Ala Lys Glu Pro Pro Gly Tyr Asn Ser Leu Pro Leu Lys Leu Leu Gly
 70 75 80
 Thr Gly Lys Ala Ile Thr Lys Leu Phe Ile Ser Val Phe Arg Thr Lys
 85 90 95
 Lys Glu Arg Lys Glu Ser Thr Met Glu Glu Lys Lys Glu Leu Thr Val

```

      100                      105                      110
Glu Lys Lys Arg Thr Pro Arg Met Glu Glu Arg Lys Glu Leu Ile Val
115                      120                      125                      130
Glu Lys Lys Lys Arg Lys Glu Ser Thr Glu Lys Thr Lys Leu Thr Lys
      135                      140                      145
Glu Glu Lys Lys Gly Lys Lys Leu Thr Lys Lys Ser Thr Lys Val Val
      150                      155                      160
Lys Lys Leu Cys Lys Val Tyr Arg Glu Gln His Ser Arg Ser Tyr Asp
      165                      170                      175
Ser Ile Glu Thr Thr Ser Thr Thr Val Leu Leu Ala Gln Thr Pro Leu
      180                      185                      190
Val Lys Cys Lys Phe Leu Tyr Asn
195                      200

```

```

<210> 464
<211> 61
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> -21...-1

```

```

<400> 464
Met Thr Phe Arg His Gln Asp Asn Ser Leu Met Phe Phe Ser Met Met
      -20                      -15                      -10
Ala Thr Cys Thr Ser Asn Val Gly Phe Thr His Thr Thr Met Asn Cys
      -5                      1                      5                      10
Ser Leu Thr Ser Pro Val Asp Phe Lys Asp Leu Leu Arg Val Leu Leu
      15                      20                      25
Ile Lys Phe Gly Tyr Asp Arg Lys Ser Thr Ile Lys Ser
      30                      35                      40

```

```

<210> 465
<211> 34
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> -19...-1

```

```

<400> 465
Met Phe Leu Lys Ser Gly Ala Gly Leu Ser Ser Cys Leu Leu Pro Leu
      -15                      -10                      -5
Cys Trp Leu Glu Arg Lys Asp His Gly Arg Arg Pro Ser Xaa His Pro
      1                      5                      10
Gly Arg
      15

```

```

<210> 466
<211> 215
<212> PRT
<213> Homo sapiens

```

```

<220>

```


<221> SIGNAL

<222> -54...-1

<400> 466

```

Met Asn Xaa Tyr Ala Ser Pro Phe Asn Xaa Gln Leu Xaa Tyr Leu Xaa
      -50      -45      -40
Leu Ser Arg Phe Glu Cys Val His Arg Asp Gly Arg Val Ile Thr Leu
      -35      -30      -25
Ser Tyr Gln Glu Gln Glu Leu Gln Asp Phe Leu Leu Ser Gln Met Ser
      -20      -15      -10
Gln His Gln Val His Ala Val Gln Gln Leu Ala Lys Val Met Gly Trp
      -5      1      5      10
Gln Val Leu Ser Phe Ser Asn His Val Gly Leu Gly Pro Ile Glu Ser
      15      20      25
Xaa Gly Asn Ala Ser Ala Ile Thr Val Ala Pro Gln Val Val Thr Met
      30      35      40
Leu Phe Gln Phe Val Met Asp Leu Lys Val Ala Ala Arg Leu Trp Phe
      45      50      55
Ser Phe Leu Val Thr Asn Val Lys Thr Phe Gln Lys Val Met Phe Tyr
      60      65      70
Lys Ile Thr Asn Gly Val Ile Phe Val Gly His Ser Lys Lys Phe Ser
      75      80      85      90
Gly Ile Lys Trp Lys Val Xaa Ile Leu Phe Ile Lys Trp Xaa Cys Leu
      95      100      105
Cys Leu His Leu Ala Leu Val Tyr Tyr Asp Phe Phe Gln Met Phe Pro
      110      115      120
Lys Xaa Val Ser Xaa Asn Phe Asp Leu Lys Cys Leu Gln Ile Asn Tyr
      125      130      135
Lys His Lys Glu Glu Ile Thr Ser Lys Arg Val Leu Phe Leu Lys Ile
      140      145      150
Ile Ile Arg Lys Cys Phe Ile
155      160

```

<210> 467

<211> 27

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17...-1

<400> 467

```

Met Val Val His Leu Leu Tyr Ala His Leu Ser Phe Thr Ser Lys Arg
      -15      -10      -5
Ala Val Val Met Leu Lys Leu Glu Ile Thr Phe
      1      5      10

```

<210> 468

<211> 85

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<400> 468

```

Met Cys Ser His Ala Ser Met Ser Phe His Thr Leu Phe His Leu Leu
      -20                      -15                      -10
Phe Leu Pro His Tyr Ile Glu Thr Phe Lys Pro Gln Ser Lys His Cys
      -5                      1                      5
Phe Phe Trp Ile Ala Ala Phe Leu Thr Ser Leu Leu Thr Pro Gln Ser
      10                      15                      20
Leu Gln Gly Phe His Ser Ser Leu Cys Ala Leu Arg Ser Gln His Phe
25                      30                      35                      40
Pro Ser Thr Cys Asn Cys Phe Cys Tyr Leu Thr Ile Ile Ala Leu Xaa
      45                      50                      55
Tyr Trp Asp Asn Leu
      60

```

```

<210> 469
<211> 51
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> -16...-1

```

```

<400> 469
Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala
      -15                      -10                      -5
Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu
1                      5                      10                      15
Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly Asn Val Leu Gln Leu
      20                      25                      30
Pro Asn Phe
      35

```

```

<210> 470
<211> 67
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> -43...-1

```

```

<400> 470
Met Thr Pro Gln Tyr Leu Pro His Gly Gly Lys Tyr Gln Val Leu Gly
      -40                      -35                      -30
Asp Tyr Ser Leu Ala Val Val Phe Pro Leu His Phe Ser Asp Leu Ile
      -25                      -20                      -15
Ser Val Leu Tyr Leu Ile Pro Lys Thr Leu Thr Thr Asn Thr Ala Val
      -10                      -5                      1                      5
Lys His Ser Ile Gln Lys Asn Cys Met Xaa Leu Val Leu Gly Lys Leu
      10                      15                      20
Leu Ser Gln

```

```

<210> 471
<211> 63
<212> PRT
<213> Homo sapiens

```

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 471
 Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Arg Ala Leu
 -15 -10 -5 1
 Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser Glu Lys His Arg
 5 10 15
 Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser Ala Pro Gly Ser
 20 25 30
 Thr Gln His Arg Arg Lys Thr Thr Arg Arg Asn Tyr Ser Ser Ala
 35 40 45

<210> 472
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -58...-1

<400> 472
 Met Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His
 -55 -50 -45
 Ser Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu
 -40 -35 -30
 Ile Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile
 -25 -20 -15
 Leu Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala
 -10 -5 1 5
 Thr Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly
 10 15 20
 Ala Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ile
 25 30 35
 Tyr Thr Leu Pro Trp Leu Leu Gln Leu Phe His Ser Thr Ala Leu Xaa
 40 45 50
 Xaa Xaa Gln Gln Pro Asn Gly Ser Leu Ser Leu Asn Ile Ser Ser Ser
 55 60 65 70
 His Ala Pro Xaa Pro Xaa Thr Cys Thr Leu Glu Pro Gly Val Asp Pro
 75 80 85
 Thr Arg Xaa Val Cys Ile Asn Pro His Pro Pro Pro Pro Ile Leu Lys
 90 95 100
 Xaa Pro Leu Ser Pro Tyr Pro Lys Pro Gln Leu Gly Thr His Ala Gly
 105 110 115
 Gln Val Asn
 120

<210> 473
 <211> 238
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -71...-1

<400> 473

```

Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg Arg
  -70                      -65                      -60
Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu Ile
-55                      -50                      -45                      -40
Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu Trp
                      -35                      -30                      -25
Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser Phe Leu Leu
                      -20                      -15                      -10
Leu Leu Ala Gly Leu Ile Ala Thr Tyr Tyr Val Glu Gly Val His Gln
  -5                      1                      5
Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr Ala Tyr Trp
10                      15                      20                      25
Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr Gly Leu His
                      30                      35                      40
Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val Thr Leu Ala
                      45                      50                      55
Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro Tyr Pro Asp
                      60                      65                      70
Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr Ile Ser Leu
75                      80                      85
Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met Trp Gly Ile
90                      95                      100                      105
Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala Arg Ala Ala
                      110                      115                      120
Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln Glu Phe Glu
                      125                      130                      135
Glu Met Leu Glu His Ala Glu Ser Ala Gln Val Arg Thr Val Gly Ile
140                      145                      150
Glu Asn Arg Thr Leu Tyr Phe Leu Lys Arg Leu Leu Arg
155                      160                      165

```

<210> 474

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37...-1

<400> 474

```

Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe
  -35                      -30                      -25
Gln His Gln Gly Ala Val Glu Leu Leu Val Phe Asn Phe Leu Leu Ile
-20                      -15                      -10
Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe
-5                      1                      5                      10
Leu His Glu Thr Gly Gly Ala Met Val Tyr Gly Leu Xaa Met Gly Leu
15                      20                      25
Ile Leu Xaa Tyr Ala Thr Ala Pro Thr Asp Ile Glu Ser Gly Xaa Val
30                      35                      40
Tyr Asp Cys Val Lys Leu Thr Phe Ser Pro Ser Thr Leu Leu Val Asn
45                      50                      55
Ile Thr Asp Gln Val Tyr Glu Tyr Lys Tyr Lys Arg Glu Ile Ser Gln
60                      65                      70                      75
His Xaa Ile Asn Pro His Xaa Gly Asn Ala Ile Leu Glu Lys Met Thr
80                      85                      90
Phe Asp Pro Xaa Ile Phe Phe Asn Val Leu Leu Pro Pro Ile Ile Phe

```

95 100 105
 His Ala Gly Tyr Ser Leu Lys Lys Arg His Phe Phe Gln Asn Leu Gly
 110 115 120
 Ser Ile Leu Thr Tyr Ala Phe Leu Gly Thr Ala Ile Ser Cys Ile Val
 125 130 135
 Ile Gly
 140

<210> 475
 <211> 96
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 475
 Met Ser Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys Leu
 -20 -15 -10
 Trp Lys Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu Leu
 -5 1 5 10
 Lys Cys Leu Leu Asp Lys Ala His Cys Val Leu Leu Thr Pro Cys Gly
 15 20 25
 Tyr Ile Phe Ser Leu Ile Ser Pro Glu Ile Leu Lys Leu Thr Leu Ile
 30 35 40
 Thr Leu Xaa Ile Leu Leu Ile Leu Lys Asn Leu His Leu Leu Trp Leu
 45 50 55
 Thr Val Ser Ser Xaa Cys Val His Arg Ser Ser Ala Arg Lys Glu Lys
 60 65 70 75

<210> 476
 <211> 41
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 476
 Met His Thr Phe Ala Asn Asp Arg Gly Leu Tyr Arg Ile Leu Leu Leu
 -20 -15 -10
 His Phe Tyr Cys Leu Leu Arg Ser Ser Glu Tyr Ile Leu Gly Tyr Lys
 -5 1 5
 Val Leu Gly Val Phe Phe Pro Ile Leu
 10 15

<210> 477
 <211> 113
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 477

Met Arg Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu
 -25 -20 -15
 Leu Phe Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His
 -10 -5 1 5
 Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu
 10 15 20
 Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn
 25 30 35
 Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys
 40 45 50
 Pro Asn Val His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys
 55 60 65
 Pro Arg Cys Pro Glu Asp Ser Leu Pro Pro Val Asn Asn Xaa Val Thr
 70 75 80 85
 Ser

<210> 478

<211> 250

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -18...-1

<400> 478

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
 -15 -10 -5
 Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser
 1 5 10
 Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
 15 20 25 30
 Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
 35 40 45
 Lys Pro Arg Tyr Ile Xaa His Leu Gly Gln His Asn Leu Gln Lys Glu
 50 55 60
 Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro
 65 70 75
 Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp Xaa Xaa Asn Asp Ile Met
 80 85 90
 Leu Val Xaa Met Xaa Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro
 95 100 105 110
 Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile
 115 120 125
 Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr
 130 135 140
 Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn
 145 150 155
 Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln
 160 165 170
 Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
 175 180 185 190
 Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys
 195 200 205
 Ala Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
 210 215 220
 Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
 225 230

<210> 479
 <211> 151
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 479
 Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr Ala Ala Val
 -20 -15 -10
 Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile
 -5 1 5 10
 Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu
 15 20 25
 Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala
 30 35 40
 Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp
 45 50 55
 Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val
 60 65 70 75
 Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ala Arg
 80 85 90
 Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val Arg Ala Ile
 95 100 105
 Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe Arg Thr Asn
 110 115 120
 Gly Lys Val Lys Ser Phe Lys
 125 130

<210> 480
 <211> 239
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 480
 Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
 -25 -20 -15 -10
 Leu Leu Gly Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
 -5 1 5
 Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
 10 15 20
 Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
 25 30 35
 Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
 40 45 50 55
 Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
 60 65 70
 Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala
 75 80 85
 Gly Arg Gln Gln Lys Lys Lys Ile Glu Arg Xaa Xaa Xaa Xaa Leu Xaa
 90 95 100

```

Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala
  105                      110                      115
Ile Gly Phe Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser Ile Phe
120                      125                      130                      135
Asp Gly Arg Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser Xaa Xaa
                      140                      145                      150
Xaa Gly Leu Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr Asp Cys
                      155                      160                      165
Ser Phe Ile Phe Leu Xaa Ile Leu Cys Thr Met Ser Ile Arg Gln Asn
                      170                      175                      180
Ile Gln Lys Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr Lys Gln
                      185                      190                      195
Ala Gly Gly Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe Ser
200                      205                      210

```

```

<210> 481
<211> 208
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> -92...-1

```

```

<400> 481
Met Arg Glu Pro Gln Lys Arg Thr Ala Thr Ile Ala Lys Xaa Xaa Ala
  -90                      -85                      -80
Xaa Glu Gly Leu Arg Asp Pro Tyr Gly Arg Leu Cys Gly Ser Glu His
  -75                      -70                      -65
Pro Arg Arg Pro Pro Glu Arg Pro Glu Glu Asp Pro Ser Thr Pro Glu
-60                      -55                      -50                      -45
Glu Ala Ser Thr Thr Pro Glu Glu Ala Ser Ser Thr Ala Gln Ala Gln
                      -40                      -35                      -30
Lys Pro Ser Val Pro Arg Ser Asn Phe Gln Gly Thr Lys Lys Ser Leu
                      -25                      -20                      -15
Leu Met Ser Ile Leu Ala Leu Ile Phe Ile Met Gly Asn Ser Ala Lys
                      -10                      -5                      1
Glu Ala Leu Val Trp Lys Val Leu Gly Lys Leu Gly Met Gln Pro Gly
5                      10                      15                      20
Arg Xaa His Ser Ile Phe Gly Asp Pro Lys Lys Ile Val Thr Glu Xaa
                      25                      30                      35
Phe Val Arg Arg Gly Tyr Leu Ile Tyr Xaa Pro Val Pro Arg Xaa Ser
                      40                      45                      50
Pro Val Glu Tyr Xaa Phe Phe Trp Gly Pro Arg Ala His Val Glu Ser
                      55                      60                      65
Ser Xaa Leu Lys Xaa Xaa His Phe Val Ala Arg Val Arg Asn Arg Cys
                      70                      75                      80
Ser Lys Asp Trp Pro Cys Asn Tyr Asp Trp Asp Ser Asp Asp Ala
85                      90                      95                      100
Glu Val Glu Ala Ile Leu Asn Ser Gly Ala Xaa Gly Tyr Ser Ala Pro
                      105                      110                      115

```

```

<210> 482
<211> 86
<212> PRT
<213> Homo sapiens

```

```

<220>

```


<221> SIGNAL

<222> -39...-1

<400> 482

Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg Val
 -35 -30 -25
 Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
 -20 -15 -10
 Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
 -5 1 5
 Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
 10 15 20 25
 His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 30 35 40
 Arg Leu Leu Thr His Trp
 45

<210> 483

<211> 40

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27...-1

<400> 483

Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
 -25 -20 -15
 Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
 -10 -5 1 5
 Leu Ser Leu Arg Ser Ala Met Ser
 10

<210> 484

<211> 65

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 484

Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp Gly
 -15 -10 -5
 Leu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr Met
 1 5 10 15
 Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Lys Lys
 20 25 30
 Lys Ile Phe Leu Phe Tyr Ala Phe Xaa Gly Cys Xaa Phe Gln Ser Ala
 35 40 45
 Thr

<210> 485

<211> 130

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -55...-1

<400> 485

```

Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln Pro Leu
-55                      -50                      -45                      -40
Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg
                      -35                      -30                      -25
Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile
                      -20                      -15                      -10
Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr
                      -5                      1                      5
Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu Ala Val
10                      15                      20                      25
Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Xaa
                      30                      35                      40
Xaa Cys Val Cys Ser Asn Phe Thr Glu Gly Pro His Leu Glu Gly Arg
                      45                      50                      55
Pro Asp Gly Asp His Ser Gly Pro Ser Glu Leu Leu Thr Gln Gly Trp
                      60                      65                      70
Ala Leu
75

```

<210> 486

<211> 209

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -84...-1

<400> 486

```

Met Val Asn Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu
                      -80                      -75                      -70
Met Leu Val Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr
                      -65                      -60                      -55
Ser Asp Thr Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly
                      -50                      -45                      -40
Thr Cys Phe Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu
                      -35                      -30                      -25
Ala Tyr Leu Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu
-20                      -15                      -10                      -5
Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr
                      1                      5                      10
Asn Ile His Leu Arg Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly
15                      20                      25
Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val
30                      35                      40
Gly Pro Thr Xaa Arg Xaa Leu Leu Cys Gly Thr Leu Ala Ala Leu His
45                      50                      55                      60
Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys Xaa Val Xaa
                      65                      70                      75
Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg
80                      85                      90
Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr

```

Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser
95 100 105
110 115 120
His
125

```
<210> 487
<211> 36
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -17..-1
```

```

<400> 487
Met Gly Trp Gln Arg Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser
      -15          -10          -5
Ala His Pro Pro Gln Gly Leu Gln Ala Gln Phe Ser Cys Cys Pro Trp
      1              5              10              15
Val Gly Ile Cys

```

```
<210> 488
<211> 44
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -29...-1
```

```

<400> 488
Met Met Ser Ser Glu Leu Arg Arg Asn Pro His Phe Leu Lys Ser Asn
          -25                      -20                      -15
Leu Phe Leu Gln Leu Leu Val Ser His Glu Ile Val Cys Ala Thr Glu
          -10                      -5                      1
Thr Val Thr Thr Asn Phe Leu Arg His Glu Lys Ala
      5              10              15

```

```
<210> 489
<211> 163
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -52..-1
```

```

<400> 489
Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala Pro Ser
      -50                      -45                      -40
Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val Arg Asp
      -35                      -30                      -25
Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg Leu Glu
-20                      -15                      -10                      -5
Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg Ala Ala

```

```

      1           5           10
Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val Pro Gly
      15           20           25
Leu His Gln Leu Thr Lys Leu Xaa Phe Leu Gln Thr Glu Asp Ser Trp
      30           35           40
Val Pro Xaa Ser Pro Asp Thr Gly Leu Xaa Pro Leu Thr Val Arg Arg
      45           50           55           60
His Val Pro Ala Xaa Trp Val Leu Leu Xaa Arg Asp Pro Leu Asp Pro
      65           70           75
Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu Gly Ser
      80           85           90
Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Xaa Lys Arg Ala Xaa Xaa
      95           100           105
Thr Arg Ser
      110

```

<210> 490
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47...-1

```

<400> 490
Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly
      -45           -40           -35
Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser
      -30           -25           -20
Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe
      -15           -10           -5           1
Pro Asp Leu Pro Thr Glu Met Pro Leu Xaa Ala Lys Gly Xaa Asn Thr
      5           10           15

```

<210> 491
 <211> 218
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -50...-1

```

<400> 491
Met His His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
      -50           -45           -40           -35
Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
      -30           -25           -20
Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
      -15           -10           -5
Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
      1           5           10
Ser Gln Asp Leu Ser Gly Gln Thr Ala Lys Lys Tyr Ala Val Ser Ser
      15           20           25           30
Arg His Asn Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Xaa Lys Gln
      35           40           45
Xaa Leu Lys Val Ser Ser Glu Asn Ser Asn Pro Xaa Gln Asp Leu Lys

```

```

      50      55      60
Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Lys Gly Ser Glu Asn Ser
      65      70      75
Gln Pro Glu Glu Met Ser Gln Glu Pro Glu Ile Asn Xaa Gly Gly Asp
      80      85      90
Arg Lys Val Glu Xaa Xaa Met Lys Lys His Gly Ser Xaa His Met Gly
95      100      105      110
Phe Pro Xaa Asn Leu Xaa Asn Gly Ala Thr Ala Asp Asn Gly Asp Asp
      115      120      125
Gly Leu Ile Pro Pro Xaa Lys Xaa Xaa Thr Pro Glu Ser Xaa Gln Phe
      130      135      140
Pro Asp Thr Glu Asn Glu Gln Tyr His Arg Asp Phe Ser Gly His Pro
      145      150      155
Xaa Phe Pro Thr Thr Leu Pro Ile Lys Gln
      160      165

```

<210> 492
 <211> 216
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

```

<400> 492
Met Val Cys Val Leu Val Leu Ala Ala Ala Ala Gly Ala Val Ala Val
-15      -10      -5      1
Phe Leu Ile Leu Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr
      5      10      15
Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His
      20      25      30
Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser
      35      40      45
Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met Ser Ala Asn Lys
50      55      60      65
Ile Asn Ser Phe Glu Leu Xaa Arg Xaa Asp Arg Xaa Pro Ser Asn Met
      70      75      80
Xaa Thr Lys Tyr Tyr Ile His Arg Ile Pro Xaa Ser Arg Glu Val Gln
      85      90      95
Gln Ser Trp Pro Ser Thr Val Xaa Thr Thr Leu His Ser Met Trp Leu
      100      105      110
Ser Xaa Pro Leu Ile His Arg Val Lys Pro Xaa Leu Val Leu Cys Asn
      115      120      125
Gly Pro Gly Thr Cys Val Pro Ile Cys Val Ser Ala Leu Leu Leu Gly
130      135      140      145
Ile Leu Gly Ile Lys Lys Val Ile Ile Val Tyr Val Glu Ser Ile Cys
      150      155      160
Arg Val Lys Thr Leu Ser Met Ser Gly Lys Ile Leu Phe His Leu Ser
      165      170      175
Asn Tyr Phe Ile Val Gln Trp Pro Ala Leu Lys Glu Lys Tyr Pro Lys
      180      185      190
Ser Val Tyr Leu Gly Arg Ile Val
      195      200

```

<210> 493
 <211> 134
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<400> 493

```

Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly
      -15      -10      -5
Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Thr
      1      5      10
Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Xaa His Pro Glu Ala
      15      20      25
Gln Glu Ala Leu Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu Ile
      30      35      40      45
Asp Arg Glu Asn Phe Val Asp Ile Val Xaa Ala Lys Leu Lys Ile Pro
      50      55      60
Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser Arg
      65      70      75
Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu Leu
      80      85      90
Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn Gly
      95      100      105
Asp Glu Val Lys Lys Glu
110      115

```

<210> 494

<211> 85

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 494

```

Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp Gly
      -15      -10      -5
Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu Asn
      1      5      10      15
Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe Gly
      20      25      30
Lys Arg Glu Gln Ala Glu Glu Glu Arg Tyr Phe Arg Ala Gln Ser Thr
      35      40      45
Glu Gln Leu Ala Xaa Leu Lys Lys Xaa His Glu Glu Glu Ile Val His
      50      55      60
His Arg Glu Gly Asp
65

```

<210> 495

<211> 292

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -29...-1

<400> 495

```

Met His Gly Leu Leu His Tyr Leu Phe His Thr Arg Asn His Thr Phe
      -25                      -20                      -15
Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr Thr Glu Tyr Thr
      -10                      -5                      1
Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu Ser Leu His Tyr
      5                      10                      15
Leu Leu Leu Pro Tyr Leu Leu Leu Gly Val Asn Leu Phe Phe Phe Thr
      20                      25                      30                      35
Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu Leu
      40                      45                      50
Leu Phe Leu His Val Tyr Glu Phe Asp Glu Xaa Met Phe Pro Lys Asn
      55                      60                      65
Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala Arg Ser Xaa His
      70                      75                      80
Cys Xaa Val Cys Asn Trp Cys Val His Arg Phe Xaa His His Cys Val
      85                      90                      95
Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg Xaa Phe Leu Ile
      100                      105                      110                      115
Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val Ala Ile Val Ser
      120                      125                      130
Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp Leu Tyr Gln Glu
      135                      140                      145
Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met Asp Thr Val Phe
      150                      155                      160
Leu Ile Gln Tyr Leu Phe Leu Thr Phe Pro Arg Ile Val Phe Met Leu
      165                      170                      175
Gly Phe Val Val Val Leu Xaa Phe Leu Leu Gly Gly Tyr Leu Leu Phe
      180                      185                      190                      195
Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr Arg
      200                      205                      210
Xaa Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val Ala Trp Pro Pro
      215                      220                      225
Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser His Gly Leu Arg
      230                      235                      240
Xaa Asn Leu Gln Glu Ile Phe Leu Pro Ala Phe Pro Cys His Glu Arg
      245                      250                      255
Lys Lys Gln Glu
260

```

<210> 496

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -56...-1

<400> 496

```

Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser
      -55                      -50                      -45
Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn Pro Ser
      -40                      -35                      -30                      -25
Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro
      -20                      -15                      -10
Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Xaa Leu Thr Gly
      -5                      1                      5
Pro Xaa Thr Asp Gly Ile Pro Phe Ala Leu Xaa Ser Ala Ala Gly Pro
      10                      15                      20

```

Phe Cys Ala Ser Phe Pro Ser Gly Xaa Leu Ser Pro Pro Gly Pro Leu
 25 30 35 40
 Pro Gly Val Arg Gly Leu Pro Leu Pro Ser Val Phe Tyr Ser Cys Gly
 45 50 55
 Ala His Pro Lys Val Leu Lys Val Ala Leu
 60 65

<210> 497
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 497
 Met Leu Xaa Leu Ser Arg Ala Thr Lys Xaa Gly Arg Ala Arg Trp Leu
 -25 -20 -15
 Met Pro Val Ile Pro Ala Leu Gln Glu Ala Xaa Ala Gly Gly Ser Arg
 -10 -5 1
 Gly Gln Glu Phe Glu Thr Ser Leu Ala Asn Met Glu Thr Glu Ala Gly
 5 10 15 20
 Glu Leu Leu Lys Pro Arg Arg Arg Arg Leu Gln
 25 30

<210> 498
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 498
 Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg Arg Pro
 -10 -5 1
 Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu Ala His
 5 10 15
 Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys Trp Arg
 20 25 30 35
 Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn Ser Ser
 40 45 50
 Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr Pro Met
 55 60 65
 Arg Arg Ser Ser Cys His Leu Glu Cys Xaa Val Ile Phe Leu Leu Gly
 70 75 80
 Arg Gln Leu
 85

<210> 499
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -13...-1

<400> 499

```

Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg Arg Pro
      -10                -5                1
Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu Ala His
  5                10                15
Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys Trp Arg
20                25                30                35
Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn Ser Ser
      40                45                50
Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr Pro Met
      55                60                65
Arg Arg Ser Ser Cys His Leu Xaa Cys Gln Val Ile Phe Leu Leu Gly
      70                75                80
Arg Gln Leu
      85

```

<210> 500

<211> 108

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<400> 500

```

Met Ser Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala
-25                -20                -15                -10
Val Thr Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys
      -5                1                5
Arg Phe Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His
      10                15                20
Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp
      25                30                35
Leu Gly Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe
      40                45                50                55
Pro Phe Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp
      60                65                70
Asn Val Gly Pro Leu Ile Ile Lys Lys Lys Glu Thr
      75                80

```

<210> 501

<211> 183

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15...-1

<400> 501

```

Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp
-15                -10                -5                1
Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu

```

```

      5      10      15
Gln Gly Arg Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
      20      25      30
His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro Thr Val Leu Gly Leu
      35      40      45
Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys Phe Ser Ala Gly Asn
      50      55      60      65
Tyr Tyr Asn Gln Gly Glu Thr Arg Lys Lys Glu Leu Leu Gln Ser Cys
      70      75      80
Asp Val Leu Gly Ile Pro Leu Ser Ser Val Met Ile Ile Asp Asn Arg
      85      90      95
Asp Phe Pro Xaa Asp Pro Gly Met Gln Trp Asp Thr Xaa His Val Ala
      100      105      110
Xaa Val Leu Leu Gln His Ile Glu Val Asn Gly Ile Asn Leu Val Val
      115      120      125
Thr Phe Asp Ala Gly Gly Xaa Ser Gly His Ser Asn His Ile Ala Leu
      130      135      140      145
Tyr Ala Ala Val Arg Lys Leu Glu Gly Gln Ile Cys Lys Pro Cys Gly
      150      155      160
Thr Gly Gln Asp Phe Lys Glu
      165

```

<210> 502
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

```

<400> 502
Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp
-15      -10      -5      1
Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu
      5      10      15
Gln Gly Xaa Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
      20      25      30
His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro Thr Val Leu Gly Leu
      35      40      45
Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys Phe Ser Ala Val Phe
      50      55      60      65
Arg Arg Glu Leu Ser Glu Tyr Thr Glu Xaa Leu Thr Ser Glu Pro Leu
      70      75      80
Xaa Ala

```

<210> 503
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -57...-1

```

<400> 503
Met Asp Val Thr Gly Asp Glu Glu Glu Glu Ile Lys Gln Glu Ile Asn
-55      -50      -45

```

```

Met Leu Lys Lys Tyr Ser His His Arg Asn Ile Ala Thr Tyr Tyr Gly
  -40          -35          -30
Ala Phe Ile Lys Lys Asn Pro Pro Gly Met Asp Asp Gln Leu Trp Leu
  -25          -20          -15          -10
Val Met Glu Phe Cys Gly Ala Gly Ser Val Thr Asp Leu Ile Lys Asn
          -5          1          5
Thr Lys Gly Asn Thr Leu Lys Glu Glu Trp Ile Ala Tyr Ile Cys Xaa
  10          15          20
Glu Ile Leu Arg Gly Leu Xaa His Leu His Gln His Lys Val Ile His
  25          30          35
Arg Xaa Ile Lys Gly Gln Asn Val Leu Leu Thr Glu Asn Ala Glu Val
  40          45          50          55
Lys Leu Val Asp Phe Gly Xaa Xaa Ala Gln Leu Asp Arg Thr Val Gly
          60          65          70
Arg Xaa Asn Thr Phe Ile Gly Thr Pro Tyr Trp Met Ala Pro Xaa Val
          75          80          85
Ile Ala Cys Asp Glu Asn Pro Xaa Ala Thr Tyr Asp Phe Lys Xaa Asp
          90          95          100
Leu Trp Ser Leu Gly Ile Thr Ala Ile Glu Met Ala Glu Gly Leu Pro
  105          110          115
Leu Ser Val Thr Cys Thr Pro
120          125

```

<210> 504
 <211> 140
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

```

<400> 504
Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
          -10          -5          1
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
  5          10          15
Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp
  20          25          30
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Ala
  35          40          45          50
Leu Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
          55          60          65
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
          70          75          80
Xaa His Gln Glu Met Val Leu Ile Leu Ser Arg His Pro Trp Ile Leu
          85          90          95
Trp Ile Thr Glu Leu Thr Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys
  100          105          110
Ser Leu Cys Glu Asn Glu Leu Trp Thr Ser Leu Tyr
115          120          125

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<210> 505
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -14...-1

<400> 505

Met Ala Ala Leu Val Thr Val Leu Phe Thr Gly Val Arg Arg Leu His
 -10 -5 1
 Cys Ser Ala Xaa Leu Gly Arg Ala Ala Ser Gly Xaa Tyr Ser Arg Asn
 5 10 15
 Trp Leu Pro Thr Pro Pro Ala Thr Gly Pro Leu Pro Ser Ser Gln Thr
 20 25 30
 Gly His Met Arg Met Ala Ala Leu Leu Pro Gln
 35 40 45

<210> 506

<211> 101

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -36...-1

<400> 506

Met Gly Pro Tyr Asn Val Ala Val Pro Ser Asp Val Ser His Ala Arg
 -35 -30 -25
 Phe Tyr Phe Leu Phe His Arg Pro Leu Arg Leu Leu Asn Leu Leu Ile
 -20 -15 -10 -5
 Leu Ile Glu Gly Ser Val Val Phe Tyr Gln Leu Tyr Ser Leu Leu Arg
 1 5 10
 Ser Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu Ile Leu Phe Cys
 15 20 25
 Asn Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg Xaa Xaa Leu Gly
 30 35 40
 Arg Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu Lys Ala Asn Xaa
 45 50 55 60
 Ala Ala Ser Xaa Gln
 65

<210> 507

<211> 341

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -55...-1

<400> 507

Met Arg Lys Val Val Leu Ile Thr Gly Ala Ser Ser Gly Ile Gly Leu
 -55 -50 -45 -40
 Ala Leu Cys Lys Arg Leu Leu Ala Glu Asp Asp Glu Leu His Leu Cys
 -35 -30 -25
 Leu Ala Cys Arg Asn Met Ser Lys Ala Glu Ala Val Cys Ala Ala Leu
 -20 -15 -10
 Leu Ala Ser His Pro Thr Ala Glu Val Thr Ile Val Gln Val Asp Val
 -5 1 5
 Ser Asn Leu Gln Ser Phe Phe Arg Ala Ser Lys Glu Leu Lys Gln Arg
 10 15 20 25

[illegible]

<210> 508

<211> 108

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42..-1

<400> 508

Met	His	Ile	Leu	Gln	Leu	Leu	Thr	Thr	Val	Asp	Asp	Gly	Ile	Gln	Ala
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Ile	Val	His	Cys	Pro	Asp	Thr	Gly	Lys	Asp	Ile	Trp	Asn	Leu	Leu	Phe
	-25					-20					-15				
Asp	Leu	Val	Cys	His	Glu	Phe	Cys	Gln	Ser	Asp	Asp	Pro	Ala	Ile	Ile
-10					-5					1				5	
Leu	Gln	Xaa	Gln	Lys	Thr	Val	Leu	Ala	Ser	Val	Phe	Ser	Val	Leu	Ser
		10					15						20		
Ala	Ile	Tyr	Ala	Ser	Gln	Thr	Glu	Gln	Xaa	Tyr	Leu	Lys	Ile	Xaa	Lys
	25						30					35			
Gly	Asp	Gly	Gly	Ser	Gly	Ser	Lys	Gly	Arg	Pro	Xaa	Xaa	Gln	Thr	Glu
	40					45					50				
Xaa	Phe	Leu	Cys	Ile	Ser	Lys	Pro	Ser	Ser	Phe	Leu				
55					60					65					

<210> 509
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 509
 Met Glu Glu Ile Ser Ser Pro Leu Val Glu Phe Val Lys Val Leu Cys
 -25 -20 -15
 Thr Asn Gln Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala
 -10 -5 1 5
 Ser Val Arg Cys Val Glu Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser
 10 15 20
 Lys His Leu Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp
 25 30 35
 Phe Thr Phe Cys Leu Glu Phe Ser Arg His Arg Cys Gln Leu Thr Glu
 40 45 50

<210> 510
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -44...-1

<400> 510
 Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys Ile
 -40 -35 -30
 Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala Gly Ile
 -25 -20 -15
 Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala Val Val Tyr
 -10 -5 1
 Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr Cys Gly Val Phe
 5 10 15 20
 Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val Ser Asn Ala Gln Val
 25 30 35
 Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu Gly Arg Thr Gly Ala Arg
 40 45 50
 Val Trp Leu Phe Ile Gly Phe Met Leu Met Phe Gly Ser Leu Ile Ala
 55 60 65
 Ser Met Trp Ile Leu Phe Gly Ala Tyr Val Thr Gln Asn Thr Asp Val
 70 75 80
 Tyr Pro Gly Leu Ala Val Phe Phe Gln Asn Ala Leu Ile Phe Phe Ser
 85 90 95 100
 Thr Leu Ile Tyr Lys Phe Gly Arg Thr Glu Glu Leu Trp Thr
 105 110

<210> 511
 <211> 130
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 511

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Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu
      -25                      -20                      -15
Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu
      -10                      -5                      1
Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
5                      10                      15                      20
Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
      25                      30                      35
Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
      40                      45                      50
Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu
      55                      60                      65
Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu
      70                      75                      80
Thr Asp Thr Gly Ser His Glu Ser Gly Tyr Gln Ser Cys Ser Pro Gly
85                      90                      95                      100
Ile Trp

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<210> 512

<211> 199

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -62...-1

<400> 512

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Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg
      -60                      -55                      -50
Xaa Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys
      -45                      -40                      -35
Val Leu Pro His Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val
      -30                      -25                      -20                      -15
Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys
      -10                      -5                      1
Ala Ser Lys His Ala Leu Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu
      5                      10                      15
Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser Asn Ile Cys Pro Gly Pro
      20                      25                      30
Val Gln Ser Asn Ile Val Glu Asn Ser Leu Ala Gly Glu Val Thr Lys
      35                      40                      45                      50
Thr Ile Gly Asn Asn Gly Asn Gln Ser His Lys Met Thr Thr Ser Arg
      55                      60                      65
Cys Val Arg Leu Met Leu Ile Ser Met Ala Asn Asp Leu Lys Glu Val
      70                      75                      80
Trp Ile Ser Glu Gln Pro Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr
      85                      90                      95
Met Pro Thr Trp Ala Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg
      100                      105                      110
Ile Glu Asn Phe Lys Ser Gly Val Asp Ala Xaa Ser Ser Tyr Phe Lys
      115                      120                      125                      130
Ile Phe Lys Thr Lys His Asp
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<210> 513
 <211> 180
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 513
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 Ser Val Met Ala Ala Leu Thr Phe Gly Cys Phe Ile Xaa Thr Ala Phe
 -5 1 5
 Lys Asp Arg Ser Val Pro Val Arg Leu His Val Ser Arg Ile Met Leu
 10 15 20
 Lys Asn Val Glu Asp Phe Thr Gly Pro Arg Glu Arg Ser Asp Leu Gly
 25 30 35
 Phe Ile Thr Phe Asp Ile Thr Ala Asp Leu Glu Asn Ile Phe Asp Trp
 40 45 50 55
 Asn Val Lys Gln Leu Phe Leu Tyr Leu Ser Ala Glu Tyr Ser Thr Lys
 60 65 70
 Asn Asn Ala Leu Asn Gln Xaa Val Leu Trp Asp Lys Ile Val Leu Arg
 75 80 85
 Gly Asp Asn Pro Lys Leu Leu Leu Lys Asp Met Lys Thr Lys Tyr Phe
 90 95 100
 Phe Phe Asp Asp Gly Asn Gly Leu Xaa Gly Asn Arg Asn Val Thr Leu
 105 110 115
 Thr Leu Ser Trp Asn Val Val Pro Asn Ala Gly Ile Leu Pro Leu Val
 120 125 130 135
 Thr Gly Ser Gly His Val Ser Val Pro Phe Pro Asp Thr Tyr Glu Ile
 140 145 150
 Thr Lys Ser Tyr
 155

<210> 514
 <211> 120
 <212> PRT
 <213> Bos taurus

<400> 514
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 20 25 30
 Phe Val Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp Asn Ala Ile
 35 40 45
 Arg Arg Arg Pro Val Leu Leu Ala Gly Leu His Arg Gln Leu Leu Tyr
 50 55 60
 Ile Thr Ser Phe Val Phe Val Gly Tyr Tyr Leu Leu Lys Arg Gln Asp
 65 70 75 80
 Tyr Met Tyr Ala Val Arg Asp His Asp Met Phe Ser Tyr Ile Lys Ser
 85 90 95
 His Pro Glu Asp Phe Pro Glu Lys Asp Lys Lys Thr Tyr Gly Glu Val
 100 105 110
 Phe Glu Glu Phe His Pro Val Arg
 115 120

<210> 515
 <211> 1082
 <212> DNA
 <213> Homo sapiens

<400> 515
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<210> 516
 <211> 559
 <212> DNA
 <213> Homo sapiens

<400> 516
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<210> 517
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 517
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 20 25 30
 His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln Ser Thr Glu
 35 40 45

Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu His
 50 55 60
 Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val Pro
 65 70 75 80
 Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Asn Leu Cys
 85 90 95
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 100 105 110

<210> 518
 <211> 4544
 <212> DNA
 <213> Homo sapiens

<400> 518
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<210> 519

<211> 1779

<212> DNA

<213> Mus musculus

<400> 519

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